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Page

OM protein - protein search, using sw model

September 11, 2003, 17:21:03; Search time 43.7968 Seconds (without alignments) 256.908 Million cell updates/sec Run on:

US-09-853-253-2 611 1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

	Description	qhrelin precursor				hypothetical prote		conserved hypothet	motilin precursor	platelet-derived e	probable two-compo	histone H2B1 - upl	٠	probable outer mem	probable usher pro	σ	protein kinase (EC			motilin precursor	homeotic protein H	probable exported	beta-hexosaminidas	cyclopropane-fatty	hypothetical prote	T-complex protein	[qlutamate-ammonia	hypothetical prote	calcium channel pr	probable kefB prot	
SUMMARIES	QI	A59316	B59316	A33323	MSPG	T30160	C84205	D82825	JC6511	S03904	683109	T09722	B36134	F90788	G85648	S47436	JC7122	146477	I46480	S24315	S53763	AC0414	A82292	D87426	E87408	138428	AI3417	T41263	10	F70591	
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æ	Ouery Match	100.0	84.8	14.5	14.1	12.9	12.4	•	٠	11.9	•	11.8				11.3	11.3	11.3	11.3	11.2	11.2	11.2	11.1	11.1	11.0	11.0	11.0	11.0	•	10.9	
	Score	611	518	88.5	98	79	75.5	3	2	72.5	$^{\circ}$	72	71	70	70	69	69	69	69	68.5	68.5	68.5	68	99	67.5	67.5	67.5	67	67	66.5	
	Result No.		7	m	4	ហ	ø	7	œ	თ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25			28	53	

hypothetical prote hypothetical prote		hypothetical prote	DNA-directed DNA p	myelin/oligodendro	ISGF3 p91-related	DNA-binding protei	excinuclease ABC c	probable pseudouri	transaldolase (EC	protein containing	hypothetical prote	flagellar biosynth	flagellar blosynth	acriflavin resista
C75460 F86639	T08772	T43168	AB0130	S58394	149508	A54444	D75615	D71068	839870	н97088	T19542	B55546	AE0745	E69795
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10.9 485 2 10.9 575 2			_											٦
.5 10.9	.5 10.9		.5 10.9 1	10.8	10.8		10.8							٦

ALIGNMENTS

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A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Rolecule type: mcNa
A.Rolecule type: mcNa
A.Rolecule type: mcNa
A.Rolecule type: mcNa
A.Rolecule tissue stomach endocrine cells
A.Role: submitted to GenBank, June 1999
C.Comment: Ghrelin secreted by the stomach stimulates the release of spmatotropin (gr
C.Superfamily: mctilin
C.Keywords: hormone; lipoprotein; stomach
F.11-23/Domain: signal sequence #status predicted <ANT>
F.52-11//Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.52-11//Domain: carboxyl-terminal propeptide #status experimental
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B59316
dynelin procursor - rat
M.Alternate names: preproghrelin
C; Species: Rattus norvegicus (Norway rat)
C; Species: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C; Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C; Accession: B59316
R; Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A; Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach. A; Reference number: A59316; MUID:20067959; PMID:10604470
A; Accession: B59316
A; Status: not compared with conceptual translation
                                                                                                                                                                                                       C;Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K. Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach. A;Reference number: A59316; MuID:20067959; PMID:10604470
                                                                 ghrelin precursor - human
N:Alternate names: preproghrelin
C;Species: Homo sapiens (man)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 611; DB 1;
100.0%; Pred. No. 9.1e-55;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 117; Conservative
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RESULT 1
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Gaps

21;

Length 115;

23 51

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1 MPSPGTVCSLLLLGMLWLDLAMAGSS-----FLSPEHQRVQQRKESKKPPAKLQPRAL
                                   F;1-25/Domain: Signal sequence *status predicted <SIG>
F;26-114/Product: promotilin *status predicted <PMAT>
F;26-47/Product: motilin *status predicted <MAT>
F;26-47/Product: carboxyl-terminal propeptide *status predicted <CTP>
                                                                                                                                                                                                                            14.5%; Score 88.5; DB 1; 25.4%; Pred. No. 0.071; Live 29; Mismatches 41;
                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.4%
Matches 31; Conservative
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       Keywords: hormone
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                                                           A.Cross-reference: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A.Experimental source: strain SD; tissue stomach endocrine cells
A.Note: submitted to GenBank, June 1999
C.Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt C.Superfamily: motilin
C.Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <AMT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 1-115 <-DNA
A.Note: the authors translated the codon CAG for residue 93 as Glu
R.Yano, H.; Seino, Y.; Fujita, J.; Yamada, Y.; Inagaki, N.; Takeda, J.; Bell, G.I.; Eddy
R.Yano, H.; Seino, Y.; Fujita, J.; Yamada, Y.; Inagaki, N.; Takeda, J.; Bell, G.I.; Eddy
A.Reference number: S04489; MUD: 89289989; PMID: 2737284
A.Recession: S04489; MUD: 89289989; PMID: 2737284
A.Residues: 1-115 <-VAN
A.Residues: 1-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
C; Date: 10'Sep-1999 #sequence_revision 10'Sep-1999 #text_change 16-Jun-2000
C; Accession: A33323; 804489; 800156; A30329
C; Accession: A33323; 804489; 800156; A30329
DNA 8; 615-621, 1989
A; Title: Structure and expression of the human motilin gene.
A; Reference number: A33323; MUID:90091748; PMID:2574660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.8%; Score 518; DB 1; Length 11 Best Local Similarity 82.9%; Pred. No. 2.4e-45; Matches 97; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Contains: motilin; promotilin
A; Molecule type: mRNA; protein
A; Residues: 1-117 <KOJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 6p21.3-6p21.3
A;Introns: 39/3; 78/3; 113/1
C;Superfamily: motilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motilin precursor - human
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A; References in the state of pre-liminary
A; Molecule type: mRNA
A; Reduction type: mRNA
A; Reduces: 1-19 < RON
A; Cross-references: GB:M31219; NID:g164589; PIDN:AAA31088.1; PID:g164590
A; Cross-references: GB:M31219; NID:g164589; PIDN:AAA31088.1; PID:g164590
A; Note: the authors translated the codon AGC for residue 29 as 11e
A; Note: the authors translated the codon AGC for residue 29 as 11e
Can. J: Blochem: 51, 533-537, 1973
A; Title: Motilin, a gastric motor activity stimulating polypeptide: the complete amin
A; Recension: A90748; MUID:73184120; PMID:4706833
A; Residues: 26-28, 17, 30-38, 12, 40-47
A; Residues: 26-28, 17, 30-38, 12, 40-47
A; Reperimental source: duodenal mucosa
R; Schubert, H.; Brown, J.C.
Can. J: Blochem: 52, 7-8, 1974
A; Title: Correction to the amino acid sequence of porcine motilin.
A; Reference number: A90749; MUID:74138109; PMID:4856583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: protein

A Residues: 38-41 <SCH>

B Yajima, H.; Kauy tr.; Kawatani, H.

Chem. Soc. D Chem. Commun. 1975, 159-160, 1975

A; Title: Synthesis of the docosapeptide corresponding to the entire amino-acid sequen
A; Reference number: A92756

A; Contents: annotation
A; Note: a 22-residue peptide having the sequence and biological activity of the natur
R; Brown, J.C.; Mutt, V.; Dryburgh, J.R.

Can. J. Physiol. Pharmacol. 49, 399-405, 1971
A; Title: The further purification of motilin, a gastric motor activity stimulating po
A; Reference number: A90755; MUID:72043589; PMID:4941085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motilin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 24-Apr-1984 #sequence_revision 26-Jan-1996 #text_change 18-Jun-1999
C;Baccession: A40932; A90748; A90749; A01578
R;Bond, C,T.; Nilaver, G.; Godfrey, B.; Zimmerman, E.A.; Adelman, J.P.
Mol. Endocrinol. 2, 175-180, 1988
A;Title: Characterization of complementary deoxyribonucleic acid for precursor of por A;Reference number: A40932; MUID:88288231; PMID:2456453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: motilin, injected intravenously into dogs, stimulates motor activity in both ecretion) from the fundic gland area pouches C;Superfamily: motilin
                                                 54 AGWLRPEDGGQAEGA----EDELE-VRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-47/Product: motilin #status experimental <MAT>
F:50-119/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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conserved hypothetical protein XF0277 [imported] - xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Dacer: 18-aug-2000 #sequence_revision 20-aug-2000 #text_change 20-aug-2000
C;Accession: D82825
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Residues: 1-709 cSIMA
A; Residues: 1-709 cSIMA
A; Residues: 1-709 cSIMA
A; Coss-references: GB: AE003881; GB: AE003849; NID: g9105093; PIDN: AAF83090.1; GSPDB:GN
A; Experimental source: Strainary
A; Experimental source: Strainary
Briones, M.E.; Bueno, M.E.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madelra, A.M.B.N.; Madelra, H.M.F.; Marlino, C.L.; Marques, M.V.; Martins
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
F.G.; Nunes, L.R.; Oliveira, M.J. de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                motilin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 19-Jan-2001
C;Accession: JC6511
R;De Clercq, P.; Depoortere, I.; Peeters, T.
Gene 202, 187-191, 1997
A;Tille: Isolation and sequencing of the cDNA encoding the motilin precursor from she A;Reference number: JC6511; MUID:98087436; PMID:9427564
-----LSPEHQRVQQRKESKKPPAKLQPRALA--GWLRPEDGGQAEGAEDELEVRFNA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 FSIAAIVMAPRHLEGKLTKFEPPPPS---PRAIAAEGWWK-NDWRQLPARRNEFDDAERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : || | || || || || 422 GALASLIGFARLYLGAHWLSDVLGGMLFGIFWLLVLGIAYRRRLTHELQVNPLSWLFYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                89 VOYOQHSQALGKFLQD 104
                                                                                                                                                                                                                       131 VKYDGDEEVYGDIIID 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
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Matches 36; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-115 <DEA>
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                                             78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C37A2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30160
R;Le, T.T.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C37A2.
A;Reference number: 220746
A;Reference number: 220746
A;Reference number: 220746
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary;
A;Residues: 1-124 < LEF>
A;Residues: 1-124 < LEF>
A;Cross-references: EMBL:U97194; PIDN:AAB52447.1; GSPDB:GN00019; CESP:C37A2.2
A;Experimental source: strain Bristol N2; clone C37A2
C;Genetics:
A;Gene: CESP:C37A2.2
A;Map position: 1
A;Introns: 46/1; 124/1; 159/1; 231/1; 508/3; 740/3; 891/1; 931/1; 975/1; 1014/3; 1083/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Vng0468c [imported] - Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Golf #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: C84205
R; NG W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: C84205
A; Accession: C84205
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C;Genetics:
A;Gene: VNG0468C
                                                                                                                                                                                  82
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                                                                                                                                                                                                                                29 SFTYGELORMOEKERNKGOKKSLSVQQASEELGPLDPSEPTKEEERVVIKLLAPVDIGIR 88
                                                                                                                                                                         26 SFLSPEHORVQORKESKKPPAKLOPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIK
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    DB 1; Length 119;
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Best Local Similarity 27.6%; Pred. No. 9;
Matches 32; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.4%; Score 75.5; DB
Best Local Similarity 30.3%; Pred. No. 6;
Matches 23; Conservative 9; Mismatches
                                                                                       19; Mismatches
14.1%; Score 86; 26.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                   86 LSGVQYQQHSQALGKFL 102
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                                                                                       Conservative
                                         Best Local Similarity
Matches 20; Conserv
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A; Residues: 1-410 <STO>
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    Query Match
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A;Cross-references: GB:AE004845; GB:AE004091; NID:g9950507; PIDN:AAG07681.1; GSPDB:GN A;Experimental source: strain PAO1
C;Genetics: A;Genetics: A;Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPALICRYTADLVLTYVNRTFADSLATSPE--------RLVGRRLDEWLAAED 614
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C;Accession: T09722.
R;Turley, R.B.; Parker, S.M.
Submitted to the EMBL Data Library, September 1997
A;Reference number: 216835
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C;Species: Escherichia coli
C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 08-Oct-1999
C;Accession: B36134
R;Dorrington, R.A.; Rawlings, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SPGTVCSLLL-LGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPED
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A;Experimental source: strain DPL 62; etiolated cotyledon
C;Superfamily: histone H2B
C;Keywords: DNa binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
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A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-147 <TUR>
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Pred. No. 30;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 4.3;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GGQAEGAEDELEVRFNAP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.8%; Score 72;
25.2%; Pred. No.
tive 22; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Scor.
28.7%; Pred
8; 1
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Best Local Similarity 28.77
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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es 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-922 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: G83109
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Best Local Si
Matches 28,
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B36134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Substance that the phosphory lase (EC 2.4.2.4)

Cidente: Liminate phosphory lase (EC 2.4.2.4)

CiSpecias: Homo sapiens (man)
CiSpecias: CiSpecias: Manual sapiens (manual sapiens)
Anticles: Identification of anglogenic activity and the cloning and expression of platele
Ancession: S03904: MID: 89181355; PMID: 2467210
Ancesion: S03904: MID: 89181355; PMID: 2467210
Ancesion: Loff Lists sequence, Including the amino end of the mature protein, was confine type: part of this sequence, Including the amino end of the mature protein, was confine and the salotens in the sapient of this sequence, Including the amino end of the mature protein, was confine type: mRNA
Ancession: Jud2: Assumption phosphorylase activity associated with platelet-derived endothelial of Ancession: Jud2: 24 2000
Antitle: Lossian and Ancession: Jud2: Ancession: Ance
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                                                                                                                                                                                                                                                         30 FTYGEVQRMQEKERYKG-----QKKSLSVQQRSEEVGPVDPAEPREEKQEVIKLTAPVEI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                          27 FLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELE----VRFNAPFDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PAPG-------DFSGEGSQGLPDPSPEPKQLPELIRMKRDGGRLSEADIRGFVA
                                                                                                                                            Gaps
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                                                                        Length 115;
                                                                                                                                         Indels
                                                                                                                                     33;
                                                                        DB 2;
                                                         11.9%; Score 72.5; DF
25.0%; Pred. No. 2.9;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 GMRMNSROLEKYQATLEGLLRKAL 108
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                                                                                                                                     Conservative
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Matches 30; Conserva
                                                                                          Local Similarity
wes 21; Conserv
C; Superfamily: motilin
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                                                                 Query Match
Best Local 9
                                                                                                                                     Matches
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Best Local Similarity 30.29
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Escherichia coli (strain 0157 C; Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: F90788 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001 A; Richara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Arithe: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A; Reference number: A99629; MUID:21156231; PMID:11258796
              A;Title: Characterization of the minimum replicon of the broad-host-range plasmid pTF-FG A;Reference number: A36134; MUID:91008941; PMID:2120189 A;Accession: B36134
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85648
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable outer membrane usher protein ECs1278 [imported] - Escherichia coli (strain 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable usher protein 21536 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                A;Status: preliminary
A;Status: preliminary
A;Subcloule type: DNA
A;Residues: 1-299 <DOR>
A;Residues: 1-299 <DOR>
A;Cross-references: GB:M7377; GB:M35249; NID:g154646; PIDN:AAA27382.1; PID:g154648
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 HTRINMAEVRKLETDPARLLHQRLCGWIDPGKSGKAEIDTLCGYVWPDAANDEAMKKRRQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-840 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34701.1; PID:g13360738; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRA-----LAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                       ----GAEDE-LEVRFN 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
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                                                                                                                                                                                                                                                                                                         11.6%; Score 71; DB 2; Length 299; 25.8%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 840;
                                                                                                                                                                                                                                                                                                                                                           15; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 TARKALVELAAVGWTVNEYAKGK-----WEISRPNP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 APFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAP 114
                                                                                                                                                                                                                                                                                                                                                                                                                    32 HORVQORKESK--KPPAKLQPRALAGWLRPEDGGGAE---
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Bacteriol. 172, 5697-5705, 1990
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 25.9% tes 30; Conservative
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A; Molecule type: DNA
A; Residues: 1-840 <STO>
                                                                                                                                                                                                                                                A; Genome: plasmid
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A; Gene: EC
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A;Cross-references: GB:AE005174; NID:g12514401; PIDN:AAG55651.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics: C;Genetics: A;Gene: 21536 C;Superfamily: outer membrane usher protein fimD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flagellar antigen - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 03-Nov-2000
C;Accession: S47436
R;Imboden, M.; Mueller, N.; Hemphill, A.; Mattioll, X.Y.Z.; Seebeck, T.
submitted to the EMBL Data Library, August 1994
A;Description: Repetitive proteins from the flagellar cytoskeleton of African Trypano
A;Reference number: S47436
A;Accession: S47436
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                                                                                                                                                                                                                                                                       3 SPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRA-----LAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 QRVQQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQ
                                                                                                                                                                                                                                                                                                                                                                                                         56 WLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAK 111
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                   28;
                                                                                                                                                         b; Score 70; DB 2; Length 840;b; Pred. No. 48;15; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
A; Residues: 1-411 <IMB>
A; Cross-references: EMBL:236281; NID:9530358; PID:9530359
A; Experimental source: strain stock TREU 1285
C; Superfamily: cytadherence-accessory protein hmwl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 69; DB 2;
30.2%; Pred. No. 27;
Tive 16; Mismatches 2
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Job time : 46.7968 secs
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Best Local Similarity 25.9%
Matches 30; Conservative
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US-09-990-456-268
US-09-992-268
US-09-992-293-268
US-09-991-144-268
US-09-991-144-268
US-09-991-144-268
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US-09-991-854-268
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Patent No. US20020055156A1
GERERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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      ORGANISM: Homo sapiens
   US-09-853-253-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-853-253-6
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      SEQ ID NO 5
LENGTH: 23
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Sequence 268, Appl
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237.266 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
3: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
4: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
6: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
7: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.ppp:*
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7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.ppp:*
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7: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.ppp:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-989-722-268
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US-09-989-732-268
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US-09-991-073-268
US-09-991-073-268
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 9; Lr
.nn 0%; Pred. No. 3.5e-15;
                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794, 987
FILING DATE: 27-Feb-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: DEISHOP, PAUL
TYLICANT: BISHOP, PAUL
TYLE OF INVENTION: ZSIG33-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FLING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 3:0
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGNENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09853253
Patent No. US20020005156A1
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%;
Matches 23; Conservative 0
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Best Local Similarity 100.0%;
Matches 23; Conservative 0
                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
   CITY: Seattle
                                       COUNTRY: USA
                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                       ZIP: 98102
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US-09-853-253-2
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0; Mismatches 0; Indels
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100.0%; Pred. No. 9e-16;
tive 0; Mismatches 0
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       APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 2s1933-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACER NO. USJULZUDSIDALI
FACERIAL INCORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, STEPHEN
APPLICANT: BIEPPREN, PAUL
TITLE OF INVENTION: Zalg33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SSO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sheppard, Paul O.
Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; 100.0%; Pred. No.
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Patent No. US20010041791A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%
Best Local Similarity 100.0%
Matches 23; Conservative
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Best Local Similarity 100..
SHEPPARD, PAUL
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
US-09-853-253-6
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US-09-794-987-2
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APPLICANT:
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R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089633

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08961

R APPLICATION NUMBER: 60/089801

R PILING DATE: 1998-06-18
                                                     APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
                                                                                                                                                  APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
APPLICATION NUMBER: 60/088212
APPLICATION NUMBER: 60/088212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
APPLICATION NUMBER: 60/089440
APPLICATION NUMBER: 60/089440
                                                                                                                                                                                                                                                FILING DATE: 1998-06-05
APPLICATION UNDHER: 60/088217
ALLING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090252
 APPLICATION NUMBER: 60/088029
                                       60/088030
                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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                   FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/
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                   PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US,09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
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R APPLICATION NUMBER: 60/078910

R FLING DATE: 1998-03-20

R APPLICATION NUMBER: 60/08332

R FILING DATE: 1998-04-28

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084600
52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                           Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087827
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Gurney,Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Goddard, Audrey
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Botstein, David
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APPLICANT: Mood, ALIIIam I.

APPLICANT: Wood, ALIIIam I.

TITLE OF INVENTION: Acids Encoding the Same
FILE RFERENCE: P3730p1c3
CURRENT APPLICATION WUMBER: US/09/989,723
PRIOR PILLING DATE: 1997-01-12
PRIOR PILLING DATE: 1997-10-13
PRIOR PILLING DATE: 1997-11-13
PRIOR PILLING DATE: 1997-11-13
PRIOR PILLING DATE: 1997-11-13
PRIOR PILLING DATE: 1998-02-25
PRIOR PILLING DATE: 1998-02-25
PRIOR PILLING DATE: 1998-02-25
PRIOR PILLING DATE: 1998-03-00
PRIOR PILLING DATE: 1998-03-00
PRIOR PILLING DATE: 1998-06-02
PRIOR PILLING DATE: 1998-06-03
PRIOR PILLING DATE: 1998-06-03
PRIOR PILLING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR APPLICATION NUMBER: 60/088030
                                                                                                                                                                                                                                                                                                                         Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Kljavin, Ivar J.
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Paoni, Nicholas F.
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                                                               Baker, Kevin P.
Botstein, David
                                     APPLICANT: Ashkenazi, Avi J
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             GENERAL INFORMATION:
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R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349

R APPLICATION NUMBER: 60/090355

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090439

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090431

R APPLICATION NUMBER: 60/090431

R APPLICATION NUMBER: 60/090435

R APPLICATION NUMBER: 60/090435

R APPLICATION NUMBER: 60/090435
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/09045

R APPLICATION NUMBER: 60/09045

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540

R APPLICATION NUMBER: 60/090540

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R APPLICATION NUMBER: 60/090540

R FILING DATE: 1998-06-24

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R APPLICATION NUMBER: 60/090678

R PILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090690

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R RILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25

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R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-26

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R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/09159

R APPLICATION NUMBER: 60/09159
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NR FILING DATE: 1998-07-07

NR APPLICATION NUMBER: 60/091982

NR FILING DATE: 1998-07-07

NR APPLICATION NUMBER: 60/092182

NR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
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23; Conservative
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326

PRIOR

; Sequence 268, Application US/09989723 ; Patent No. US20020072092A1

US-09-989-723-268

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PRILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/086212

R APPLICATION NUMBER: 60/086212

R APPLICATION NUMBER: 60/086217

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-09

R APPLICATION NUMBER: 60/08655

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08738

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08738

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/080738
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RAPLICATION NUMBER: 60/088824

RELING DATE: 1998-06-10

RAPLICATION NUMBER: 60/088858

RELING DATE: 1998-06-11

RAPLICATION NUMBER: 60/08858

RELING DATE: 1998-06-11

RAPLICATION NUMBER: 60/08861

RAPLICATION NUMBER: 60/08881

RAPLICATION NUMBER: 60/08881

RAPLICATION NUMBER: 60/08881
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R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089518

R APPLICATION NUMBER: 60/089518
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RELING DATE: 1998-06-17

RAPELICATION NUMBER: 60/089598

RELING DATE: 1998-06-17

RELING DATE: 1998-06-18

RAPLICATION NUMBER: 60/08961

RELING DATE: 1998-06-18

RELING DATE: 1998-06-19
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R FILING DATE: 1998-06-19
A PPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
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th 100.0%; Score 23; DB 9; Length 117; Similarity 100.0%; Pred. No. 3.5e-15; 23; Conservative 0; Mismatches 0; Indels PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR APPLICATION NUMBER: 60/090444
PRIOR PILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090535
PRIOR PELING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/09057
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091696
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-03
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1998-07-03
PRIOR PELING DATE: 1998-07-03
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1998-07-03
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091938
PRIOR PELING DATE: 1998-07-07
PRIOR PELING D Query Match Best Local Similarity Best Loc Matches

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Sequence 268, Application US/09989279; Sequence 268, Application US/09989279; Patent No. US200220072496A1; APPLICANT: APPLICANT: BAKer, Kevin P.; APPLICANT: Botstein, David; APPLICANT: Eaton, Dan L.

Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone APPLICANT

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R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/08655

R FILING DATE: 1998-06-09

R RPLING DATE: 1998-06-10

R APPLICATION NUMBER: 60/080734

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/080738

R APPLICATION NUMBER: 60/080742

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/080810

R APPLICATION NUMBER: 60/080810
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BR FILING DATE: 1998-06-11

BR FILING DATE: 1998-06-11

BR APPLICATION NUMBER: 60/089105

BR FILING DATE: 1998-06-16

BR APPLICATION NUMBER: 60/089512

BR FILING DATE: 1998-06-16

BR APPLICATION NUMBER: 60/089538

BR FILING DATE: 1998-06-17

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R APPLICATION NUMBER: 60/090349

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APPLICATION UNMBER: 60/088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-66-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/088824
APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER:: 60/090445
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730HOER: US/09/989,279
CURRENT APPLICATION NUMBER: US/09/989,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: 05/09/289, CURRENT APPLICATION NUMBER: 06/06226 PRIOR APPLICATION NUMBER: 06/06226 PRIOR APPLICATION NUMBER: 06/06226 PRIOR APPLICATION NUMBER: 06/06236 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 06/065311 PRIOR APPLICATION NUMBER: 06/06570 PRIOR APPLICATION NUMBER: 06/06770 PRIOR PELING DATE: 1998-02-25 PRIOR APPLICATION NUMBER: 06/078910 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 06/084600 PRIOR APPLICATION NUMBER: 06/084600 PRIOR FILING DATE: 1998-03-28 PRIOR APPLICATION NUMBER: 06/087607 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 06/087607 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 06/087607 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR PRILING DATE: 1998-06-03 PRIOR FILING DATE: 1998-06-03 PRIOR FILING DATE: 1998-06-03 PRIOR FILING DATE: 1998-06-04 PRIOR FILING DATE: 1998-06-06-04 PRIOR FILING DATE: 1998-06-06-04 PRIOR FILING DATE: 1998-06-06-04 PRIOR FILING DATE: 1998-06-04 PRIOR PRIOR DATE: 1998-06-04 PRIOR PRIOR DATE: 1998-06-06-04 PR
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R APPLICATION NUMBER: 60/086029

R FILING DATE: 1998-06-04

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R APPLICATION NUMBER: 60/086033

R FILING DATE: 1998-06-04

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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
                                                                                                                                                                                   Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
                                       Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F
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| WILLIE CON | INVENTION: Societed and Transmembrane Polypeptides and Nucleic TITLE ON INVENTION: Societed and Transmembrane Polypeptides and Nucleic TITLE ON INVENTION: Acids Encoding the Same FILE REPRENEW. Acids Encoding the Same FILE REPRENEW. Acids Encoding the Same FILE REPRENEW. Acids DATE: 1991-11-1999, 727
CURRENT PELLIG DATE: 1991-11-1999, 727
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PRIOR PELLIG DATE: 1999-10-209
PRIOR PELLIG DATE: 19
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/090535
PRIOR PAPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
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Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Best Local Similarity 100.0%; Pa
Matches 23; Conservative 0;
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Eaton, Dan L.
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US-09-989-727-268
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R APPLICATION NUMBER: 60/088742
RR APPLICATION NUMBER: 60/088742
RR FILING DATE: 1998-06-10
RR APPLICATION NUMBER: 60/088810
RR FILING DATE: 1998-06-10
RR APPLICATION NUMBER: 60/088824
RR APPLICATION NUMBER: 60/088826
RR APPLICATION NUMBER: 60/088826
RR FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/09035
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/089512
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089947
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
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FILING DATE: 1998-06-24
FILING DATE: 1998-06-24
PAPPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-16
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Sequence 268, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION:

US-09-989-731-268

APPLICANT: Ashkenazi, Avi J.

Baker, Kevin P. Botstein, David

APPLICANT:

Desnoyers, Luc

Eaton, Dan L.

Grimaldi, J. Christopher

Gurney, Austin L.

APPLICANT APPLICANT APPLICANT

Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.

> APPLICANT: APPLICANT: APPLICANT:

Ferrara, Napoleone

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Fong, Sherman Gerber, Hanspeter Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel

APPLICANT: APPLICANT: APPLICANT:

Pan, James Paoni, Nicholas F.

Napier, Mary A.

Kljavin, Ivar

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R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090234

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R R FILING DATE: 1998-06-23

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R FILING DATE: 1998-06-23

R R FLING DATE: 1998-06-34

R APPLICATION NUMBER: 60/090439

R R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

R FILING DATE: 1998-06-24

R R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090444

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R APPLICATION NUMBER: 60/090444

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R APPLICATION NUMBER: 60/090445
                                           R APPLICATION NUMBER: 60/08858
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-18

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R APPLICATION NUMBER: 60/089908

RR PILING DATE: 1998-06-18

R PILING DATE: 1998-06-19

R FILING DATE: 1998-06-19

R FILING DATE: 1998-06-19

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R APPLICATION NUMBER: 60/089948

R APPLICATION NUMBER: 60/089952

RR PILING DATE: 1998-06-19

RR PILING DATE: 1998-06-22

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APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090678
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          APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Sandy
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730BL70
CURRENT APPLICATION NUMBER: US/09/989,731
PRIOR PELLING DATE: 1997-0-16
PRIOR FILING DATE: 1997-0-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/08800
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087106
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08729
PRIOR APPLICATION NUMBER: 60/08729
PRIOR PILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
Watanabe, Colin K.
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR PAPLICATION NUMBER: 60/06250
PRIOR PAPLICATION NUMBER: 60/06250
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PAPLICATION NUMBER: 60/06570
PRIOR PAPLICATION NUMBER: 60/06570
PRIOR PAPLICATION NUMBER: 60/0810
PRIOR PAPLICATION NUMBER: 60/08110
PRIOR PAPLICATION NUMBER: 60/081110
PRIOR PAPLICATION NUMBER: 60/081110
PRIOR PAPLICATION NUMBER: 60/081110
PRIOR PAPLICATION NUMBER: 60/08111
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PRIOR APPLICATION NUMBER: 60/08861
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/088876
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: A Acids Encoding the Same
FILE REFERENCE: P2730PIC57
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100.0%; Pred. No. 3.5e-15;
1ve 0; Mismatches 0;
                                                                                                                                   DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090695

DR APPLICATION NUMBER: 60/090695

DR FILING DATE: 1998-06-25

DR FILING DATE: 1998-06-25

DR FILING DATE: 1998-06-25

DR FILING DATE: 1998-06-26

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/090863

DR APPLICATION NUMBER: 60/090863

DR APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

DR FILING DATE: 1998-07-01

DR FILING DATE: 1998-07-01

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091519

DR FILING DATE: 1998-07-02

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DR FILING DATE: 1998-07-03

DR FILING DATE: 1998-07-03
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NR FILING DATE: 1998-07-07

NR APPLICATION NUMBER: 60/091982

NR FILING DATE: 1998-07-07

NR APPLICATION NUMBER: 60/092182

NR FILING DATE: 1998-07-09
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Patent No. US20020123463A1
GENERAL INFORMATION:
                                                  069060/09
                                                                             FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Stewart, Timothy A.
Tumas, Daniel
Watnabe, Colin K.
Williams, P. Mickey.
                           APPLICATION NUMBER: 60/C
                    FILING DATE: 1998-06-25
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Fong, Sherman
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Paoni, Nicholas F.
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Goddard, Audrey
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Best Local Similarity 100.
Matches 23; Conservative
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Botstein, David
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PRIOR PAPLICATION NUMBER: 60/09105
PRIOR PALLICA DATE: 1998-60-10
PRIOR PALLICA DATE: 1998-60-17
PRIOR PALLICATION NUMBER: 60/09559
PRIOR PALLICA DATE: 1998-60-17
PRIOR PALLICA DATE: 1998-60-19
PRIOR PALLICA DATE: 1998-60-12
PRIOR PALLICA DATE: 199
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
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PRILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090862

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR APLICATION NUMBER: 60/091478

DR APLICATION NUMBER: 60/091544

DR APLICATION NUMBER: 60/09154

DR APLICATION NUMBER: 60/09159

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091626

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02
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Patent No. US20020177576A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerber, Hanspeter
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US-09-991-073-268
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                      PRIOR
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1997-11-12 1997-11-13 1997-11-24 NUMBER: 60/066770 1997-11-24 NUMBER: 60/075945 1998-02-25 NUMBER: 60/078910 1998-03-20 NUMBER: 60/08332 1998-04-28 1998-04-20	998-05-28 MBER: 60/08760 998-06-02 998-06-02 998-06-02 998-06-02 998-06-02 998-06-04 MBER: 60/08802 998-06-04 MBER: 60/08803 998-06-04 MBER: 60/08816 998-06-05 MBER: 60/08816 998-06-05 MBER: 60/08816 998-06-05	ER: 50/08853 ER: 60/08873 ER: 60/08873 ER: 60/08873 ER: 60/08874 ER: 60/08881 ER: 60/08882 ER: 60/08883 ER: 60/08883
PILING DATE: APPLICATION FILING DATE: APPLICATION PILING DATE: APPLICATION FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE:	LING DATE: PLICATION LING DATE	PELICATION PELICATION PELICATION PELICATION ILING DATE:
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PRIOR APPLICATION NUMBER: 60/089514
PRIOR PLICATION NUMBER: 60/089532
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PRIOR PLICATION NUMBER: 60/089599
PRIOR PLILAGATION NUMBER: 60/089599
PRIOR PLILAGATION NUMBER: 60/089599
PRIOR PLILAGATION NUMBER: 60/089509
PRIOR PLILAGATION NUMBER: 60/089609
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REFLING DATE: 1998-06-02

RAPPLICATION NUMBER: 60/08727

RAPLICATION NUMBER: 60/088021

REILING DATE: 1998-06-04

REILING DATE: 1998-06-04

REILING DATE: 1998-06-04

RAPLICATION NUMBER: 60/088025

REILING DATE: 1998-06-04

RAPLICATION NUMBER: 60/088029

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RAPLICATION NUMBER: 60/088033

REILING DATE: 1998-06-04

RAPLICATION NUMBER: 60/08803

REILING DATE: 1998-06-05

RAPLICATION NUMBER: 60/088127

REILING DATE: 1998-06-05

RAPLICATION NUMBER: 60/088127

REILING DATE: 1998-06-05

RAPLICATION NUMBER: 60/088127

REILING DATE: 1998-06-05

REILING DATE: 1998-06-10

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REILING DATE: 1998-06-10

REPLICATION NUMBER: 60/088738

REILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/088810

R APPLICATION NUMBER: 60/08884

R FILING DATE: 1998-06-10

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APPLICATION NUMBER: 60/088861
APPLICATION UNMBER: 60/088876
                                                              APPLICATION NUMBER: 60/084600 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-08 FILING DATE: 1998-05-28
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FILLING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089532
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APPLICATION UNMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
                          FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/089514
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Best Local Similarity 100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0;
              PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-01
PRIOR PRILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Av1 J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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FILING DATE: 1998-07-01
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Desnoyers, Luc
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R APPLICATION NUMBER: 60/090535
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090540
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R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/089947
R FILING DATE: 1998-06-19
R PILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/089952
R R FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
PAPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE FEFFENCE: P2130PLC7;
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06286
PRIOR PELICATION NUMBER: 60/065186
PRIOR PELICATION NUMBER: 60/06511
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-02-25
PRIOR PELICATION NUMBER: 60/078910
PRIOR PELICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020112253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/08901
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PRIOR APPLICATION NUMBER: 60/08947
PRIOR PLILING DATE: 1998-06-18
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PRIOR PLILING DATE: 1998-06-22
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PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/09025
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PRIOR PLILING DATE: 1998-06-23
PRIOR PLILING DATE: 1998-06-23
PRIOR PLILING DATE: 1998-06-23
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR PLILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PLILING DATE: 1998-07-02
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PRIOR PLILING DATE: 1998-07-02
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PRIOR PLILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091634
PRIOR PLILING DATE: 1998-07-02
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PRIOR PELLING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/08025

PRIOR PLILING DATE: 1998-06-04

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PRIOR PLILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/08953

PRIOR PLILING DATE: 1998-06-17

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APPLICANT:
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APPLICANT:
APPLICANT:
Stewart, Timothy A.
APPLICANT:
APPLICANTION:
ACID Encoding the Same
FILE REFERENCE:
FILE APPLICATION NUMBER:
60/062250
FRIOR FILING DATE:
1997-10-17
FRIOR FILING DATE:
1997-11-13
FRIOR FILING DATE:
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Pred. No. 3.5e-15;
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Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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FILING DATE: 1998-05-07
PPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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Paoni, Nicholas F.
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Eaton, Dan L.
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US-09-993-604-268
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PRIOR PLICATION NUMBER: 60/089948
PRIOR PLICATION NUMBER: 60/089952
PRIOR FLILIKO DATE: 1998-66-12
PRIOR PLILIKO DATE: 1998-66-13
PRIOR PLILICATION NUMBER: 60/090349
PRIOR PLILICATION NUMBER: 60/090349
PRIOR PLILICATION NUMBER: 60/09035
PRIOR PLILICATION NUMBER: 60/09035
PRIOR PLILIKO DATE: 1998-66-24
PRIOR PLILIKO DATE: 1998-66-24
PRIOR PLILIKO DATE: 1998-66-24
PRIOR PLILICATION NUMBER: 60/090435
PRIOR PLILICATION NUMBER: 60/090445
PRIOR PLILIKO DATE: 1998-66-24
PRIOR PLILICATION NUMBER: 60/09045
PRIOR PLILICATION NUMBER: 60/09045
PRIOR PLILICATION NUMBER: 60/09055
PRIOR PLILICATION NUMBER: 60/09065
PRIOR PLILICATION NUMBER: 60/09066
PRIOR PLILICATION NUMBER: 60/09162
PRIOR PLILICATION NUMBER: 60/09162
PRIOR PLILICATION NUMBER: 60/09163
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0; Gaps

Length 117; Indels

Query Match 100.0%; Score 23; DB 10; Best Local Similarity 100.0%; Pred. No. 3.5e-15; Matches 23; Conservative 0; Mismatches 0;

1 ALAGWLRPEDGGQAEGAEDELEV 23

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Search completed: September 11, 2003, 18:16:18 Job time : 15.1444 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 11, 2003, 17:46:37; Search time 8.73262 Seconds (without alignments) 253.289 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-853-253-5 23 1 ALAGWLRPEDGGQAEGAEDELEV 23

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283308 segs, 96168682 residues Searched:

0 Word size :

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		ع م			CHANGE	
	Score	Match	y h Length	80		Q,
	23	100.0		-	20	qhrelin precursor
	80	34.8		7	T04453	
_	7	30.4		7	JH0572	
_	7	30.4		~	A48990	G
	7	30.4	4 910	7	B83451	aconitate hydratas
	7	30.4		Н	QQBE10	BOLF1 protein - hu
_	9	26.1	9	7	C87574	cold-shock domain
œ	9		14	~	AB0401	probable membrane
_	9	26.1		~	E82118	conserved hypothet
0	9	26.1		7	A30230	quiescence-specifi
_	9	26.1		7	T46695	hypothetical prote
C)	9	26.1	_	7	A91082	
m	9	26.1	_	7	B85927	
_	φ	26.1	_	7	D69070	O
n D	9	26.1	_	7	A40866	HL-60-induced diff
	ø	26.1		7	T30002	hypothetical prote
7	9	26.1		7	A95298	
<u>~</u>	9	26.1		~	CTPGP	_
19	9	26.1	1 284	7	B25624	tropomyosin I, tho
0	9	26.1		7	A25624	tropomyosin I, emb
_	Q	26.1		Cł	A55737	PD-1 protein - hum
~	φ	26.1		~	T48894	lipoprotein mtsA,
.	ø	26.1		N	H83433	hypothetical prote
_	φ	26.1		~	H71852	
'n	Q	26.1		~	T35144	Œ
	Q	26.1		~	T48871	catechol 1,2-dioxy
_	φ	26.1		ď	F72508	
~	Q	56	1 313	~	E82762	
_	φ	26	1 315	7	F64129	probable phosphogl

26.1 326 1 E66969 transcription repr 26.1 343 2 AH1823 SIGS Thosomal protection of the complex	Arabidopsis thaliana (mouse-ear cress) svision 30-Apr-1999 #text_change 30-Apr-1999 1, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes te Database, April 1998 77 Columbia; BAC clone F4D11 1/3; 206/2; 247/2; 345/3; 395/1; 434/2
1 E69690 2 AH323 2 AH3526 2 AB3526 2 AB3526 2 AB3528 2 S59598 2 S73933 2 S73934 2 AA771 1 DCSPK 2 DGSPK 2 T47471 2 T47471 2 T47471 2 T47471 2 T47471 2 T47471 2 T6406 2 H6406 2 H6406 2 AF3633 4 AF3633 6 ALIGNMENTS ALIGNME	D11.80 - Arabidopsis the thallana (mouse-ear crequence_revision 30-Apr-Rechmann, S.; Borkova, n Sequence Database, Ag 360 L:ALO22537 cultivar Columbia; BAC ellivar Columbia; BAC
11.	- Ara (mo
26.1 326 1 E69690 26.1 343 2 AH1823 26.1 343 2 AH1823 26.1 346 2 AB3322 26.1 346 2 AB3323 26.1 346 2 AB3323 26.1 346 2 AB3223 26.1 346 2 AB3223 26.1 377 2 T47471 26.1 377 2 T47471 26.1 377 2 T47471 26.1 379 2 DB28DH 26.1 379 2 DB28DH 26.1 383 2 F83321 26.1 383 2 F83321 26.1 384 2 H64506 26.1 386 2 T26404 26.1 381 2 AF3633 26.1 381 2 AF3633 26.1 381 2 AF3633 26.1 381 2 AF3633 26.1 391 2 AF3643 26.1 391 2 AF3641 26.1 391 2 A	protein F4D11.80 - Arabid abidopsis thaliana (mouse r-1999 #sequence_revision T04453 Benes, V.; Rechmann, S.; Libe Protein Sequence Data: The Protein Sequence Data: Umber: Z15360 T04453 Pe: DNA -4483 <bev> -1483 <bev> -1585</bev></bev>
26.1 26.1 26.1 26.1 26.1 26.1 26.1 26.1	1n F4 psis 9 #se 3 / v.; rotei: 2153 ANA NA
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cold-shock domain family protein [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: 20-Apr-2001
C; Accession: C87574
E; Acce
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A;Accession: A43041
                                                                                                                                                                                                                                                                                                                                                                                GB:AE004091; NID:99947516; PIDN:AAG04951.1; GSPDB:GN
                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1239 <BAN>
A;Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24841.1; PID:91334855
K;Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Glbson, T.J.
Nature 310, 207-211, 1984
S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <STO>
A;Cross-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148
C;Genetics: A;Gene: CC2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOLFI protein - human herpesvirus 4 (strain B95-8)
C;Species; human herpesvirus 4, Epstein-Barr virus
C;Species; human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: A33041; A03752; S32995
R;Bankier, A.T.; Delninger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: human herpeavirus 4 BOLFI protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: acnA; PA1562
C;Superfamily: iron-responsive element-binding protein
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Pred. No. 33;
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v 100.0%; Pred. No. July 100.0%; Pred. No. July 100.0%; Mismatches
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                                                                                                                                                                                                         A;Accession: B03451
A;Status: prealiminary
A;Molecule type: DNA
A;Residues: 1-910 <STO>
A;Cross-references: GB:AE004584; GB:A;Cross-references: GB:AE004584; GB:A;Cross-references: GB:AE004584; GB:A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
7; Conservative
                                       .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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65 ALAGWLR 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nypothetical protein - Streptomyces lividans (fragment)
C; Species: Streptomyces lividans
C; Species: Streptomyces lividans
C; Species: Streptomyces lividans
C; Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C; Accession: JH0572
R; Lichenstein, H. S.; Busse, L. A.; Smith, G. A.; Narhi, L. O.; McGinley, M. O.; Rohde, M. F.;
R; Lichenstein, H. S.; Busse, L. A.; Smith, G. A.; Narhi, L. O.; McGinley, M. O.; Rohde, M. F.;
A; Lichenstein, H. S.; Busse, L. A.; Smith, G. A.; Narhi, L. O.; McGinley, M. O.; Rohde, M. F.;
A; Lichenstein, H. S.; Busse, L. A.; Smith, G. A.; Narhi, L. O.; McGinley, M. O.; Rohde, M. F.;
A; Reference number: JH0571; MUID:92192468; PMID:1547948
A; Accession: JH0572
A; McGession: JH0572
A;
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C;Species: Streptomyces lividans
C;Species: Streptomyces lividans
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A48990
R;Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
A;Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid
A;Reference number: A48990; MUID:93099553; PMID:1464066
A;Accession: A48990
A;Status: preliminary
A;Accession: A48990
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-344 < GUT>
A;Residues: 1-344 < GUT>
A;Residues: lequece extracted from NCBI backbone (NCBIN:121210, NCBIP:121213)
C;Superfamily: Pseudomonas putida regulatory protein catR
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C;Date: 15:Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83451
R;Stover, C:K:; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hic)
                                                                                                                                                                      Gaps
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                                                                               Length 483;
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100.0%; Pred. No. 10;
tive 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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                              Query Match
Best Local Similarity
8; Conserve
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A; Note: F4D11.80
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B83451
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A;Molecule type: mRNA
A;Residues: 1-178 <BED>
R;Dozin, B.; Descalzi, F.; Briata, L.; Hayashi, M.; Gentill, C.; Hayashi, K.; Quarto, J. Biol. Chem. 267, 2979-2985, 1992
A;Title: Expression, regulation, and tissue distribution of the Ch21 protein during c A;Reference number: A42581; MUID:92147639; PMID:1737754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aymolecule type: mRNA
A;Residues: 21-95,'L',97-178 <CAN>
A;Cass-references: GBM37611
A;Crancedda, F.D.; Asaro, D.; Mollna, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne
Biochem. Blophys. Res. Commun. 168, 933-938, 1990
A;Title: The amino terminal sequence of the developmentally regulated CH21 protein sh
A;Reference number: A35491; MUID:90267487; PMID:2346493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quiescence-specific protein precursor - chicken
N;Alternate names: Ch21 protein
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C;Accession: A30230; A42581; A36595; A35491
R;Bedard, P.A.; Yannons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A;Title: Rapid repression of quiescence-specific gene expression by epidermal growth
A;Reference number: A30230; MUID:89261749; PMID:2498647
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C;Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180
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A; Residues: 21-48 <CA2>
C; Superfamily: lipocalin; lipocalin homology
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-178/Product: quiescence-specific protein #status predicted <MAT>
F; 25-173/Domain: lipocalin homology <LIP>
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100.0%; Pred. No. 68;
:ive 0; Mismatches
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Best Local Similarity 100...
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A; Status: preliminary
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C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Versinia pestis
C; Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AB0401
R; Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Experimental source: serogroup 01; strain N16961; blotype El Tor
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R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R.Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
I. R.R.; McKalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A;Residues: 1-142 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92534.1; PID:g15981232; GSPDB:GN00175
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C; Superfamily: major cold shock protein; cold shock domain homology
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                                                                      Length 69;
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100.0%; Pred. No. 57;
iive 0; Mismatches
                                                               26.1%; Score 6; DB 2;
100.0%; Pred. No. 32;
Live 0; Mismatches
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1larity 100.0%; Pred. No. 67;
Conservative 0; Mismatches
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A,Gene: YPO3302
C,Superfamily: hypothetical protein HI0489
                             Query Match
Best Local Similarity 100..
6; Conservative
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Best Local Similarity luv..
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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GQAEGA 59
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A;Molecule type: DNA
A;Residues: 1-175 <HEI>
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A; Status: preliminary
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|130 EGAEDE 135
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Best Local Similarity
Matches 6; Conserv
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   C; Accession: D69070
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C;Species: Escherichia coll
C;Species: Bo-ui-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: A91082
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Ascession: A91082
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Residues: DNA
A;Residues: 1-189 <ARY>
A;Residues: 1-189 <ARY>
A;Residues: 1-189 <ARY>
A;Residues: 1-189 <ARY>
A;Residues: 1-180 <ARY
A;Resid
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain Delt
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
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                                   Length 180;
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                                   DB 2;
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100.0%; Pred. No. 72;
1ve 0; Mismatches
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100.0%; Pred. No. 72;
iive 0; Mismatches
                               26.1%; Score 6; DB 2
100.0%; Pred. No. 69;
tive 0; Mismatches
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Query Match
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Matches 6; Conserve
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|4 ALAGWL 19
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|4 ALAGWL 19
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Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Chucch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

N. Bacteriol. 179, 7135-7155, 1997

A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A; Reference number: A69000; MUID:98037514; PMID:9371463

A; Accession: D69070

A; Status: preliminary: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A; Cross-references: G:AED00912; GB.AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262

A; Experimental source: strain Delta H

A; Cross-references: G:AENDO0912; GB.AE000666; NID:g2622632; PIDN:AAB85999.1; PID:g262

A; Experimental source: strain Delta H

A; Genetics:

C; Genetics:
A; Start codon: TTG

C; Superfamily: amidotransferase hisH; trpG homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HL60-induced differentiation immediate-early protein ETR101 - human C; Species: Homo sapiens (man) C; Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Nov-1999 C; Accession: A40866 M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H. Shimizu, N.; Ohta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H. A.Title: Expression of a novel immediate early gene during 12-0-tetradecanoylphorbol-A; Reference number: A40866; MUID:91286224; PMID:2061303
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A,Molecule type: mRNA
A,Residues: 1-223 <SHI>
A,Cross-references: GB:M62831; NID:g182260; PIDN:AAA35814.1; PID:g182261
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September 11, 2003, 17:30:37; Search time 4.42781 Seconds (without alignments) 244.278 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    127863 seqs, 47026705 residues
                                                                                                                                                                          US-09-853-253-5
23
1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Q9ubu3 homo sapien	Q9bdj6 bos taurus	Q91127 streptomyce		P03189 epstein-bar		P21760 gallus gall	methand	P01192 s corticotr	-	9	_	Q9zk75 helicobacte	Q8p280 streptococc	streptoc	٠.		_	Q8yi74 brucella me	Q10717 zea mays (m			Q99ti6 staphylococ		P47491 mycoplasma	P78022 mycoplasma	-		P49591 homo sapien	P16098 hordeum vul	_	kix3	074261 candida alb
SUMMARIES	£		GHRL_HUMAN	GHRL_BOVIN	MPR2_STRCO	MPRR_STRLI	V120_EBV	GHRL_CANFA	EFAB_CHICK	HIS5_METTH	COLI_PIG	TPM2_DROME	PCD1_HUMAN	OPSD_LIMPA	PARB_HELPJ	MTSA_STRP8	MTSA_STRPY	MRAW_XYLFA	YF56_HAEIN	RBSR_BACSU	MRAW_BRUME	CYS2_MAIZE	PURK_BACSU	IF5_SCHPO	TIG_STAAM	CUS1_YEAST	RPSD_MYCGE	RPSD_MYCPN	SYS_MOUSE	SYS_BOVIN	SYS_HUMAN	AMYB_HORVU	Z173_HUMAN	CH60_BUCTC	HS60_CANAL
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	Ouery Match	; ;	0.0	S	4.	4.0	4.	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	9.1	6.1	6.1	6.1	26.1	6.1	26.1					7.	1.9	26.1	26.1	26.1	6.1		9.1
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P19882 saccharomyc P5012 ajellomyces O92154 coturnix co P26242 rhodobacter P51693 homo sapien P35492 mus musculu O14978 homo sapien Q92512 streptomyce O54951 mus musculu O70141 rattus norv P25516 escherichia
HS60_YEAST SM60_AJBCA SMP_COTJA DXS_RHOCA PPTL_HUMAN HUTH_MOUSE 2263_HUMAN HUTE_SARRE UVR_STRCO SM6E_MOUSE SM6E_RAT ACOL_ECOLI
572 590 620 641 651 657 683 702 728 886 890
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ALIGNMENTS

Gaps

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Indels

Length 117;

Score 23; DB 1; I Pred. No. 5.4e-17; Mismatches

100.08; 100.0%;

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23; Conservative

1 ALAGWLRPEDGGQAEGAEDELEV 23

117 AA; 12911 MW; 39C0572EBECA2755 CRC64;

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Query Match
Best Local Similarity
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                                       Matches
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                                                                                                                                                                                                                                                                                                                            DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/GhrelinID327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelabs.sib.ch).
                                                                                                                                                                      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                    Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                       TISSUE—Stomach:

MEDLINE20389976; PubMed=10930375;

MEDLINE20389976; PubMed=10930375;

Staub A., Alexander G., Chenard M.-P., Rio M.-C.;

"Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";

Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
Isola-Q9UBU3-1; Sequence=Displayed;
Name=2; Synonyms=del.Gln14-ghrelin;
Isola-Q9UBU3-2; Sequence=VSP_003245;
PTM: On-octanoylation is essential for activity.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-OCTANOATE.
Missing (in isoform 2).
/FIId=VSP_003245.
L -> M (IN REF. 5).
                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHRELIN.
                                                                                                                                                                                                                               growth regulation.
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                          MEDLINE-21203998; PubMed-11306336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AJ25278; CAB657331; --
EMBL, AF29658; AAG10300.1; --
EMBL, BC025791; AAH25791.1; --
PIR; A59316; A59316.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB029434; BAA89371.1; -. EMBL; AB035700; BAB19045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIN:
AIDDOM; PD33210.
HORmone; Cleavage c.
Alternative splicing.
CIGNAL 1 23
CTONAL 24 51
52 117
56 26
                                              SEQUENCE OF 24-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1624; GHRELIN.

Probom; PD332162; Preproghtelin; 1.

Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.

SIGNAL 24 50 GHRELIN (BY SIMILARITY).

PEPTIDE 24 50 GHRELIN (BY SIMILARITY).

PEPTIDE 51 116 REMOVED IN MATURE FORM (BY SIMILARITY).

LIPID 26 N-NCCTANOATE (BY SIMILARITY).

CONFLICT 34 4 K -> E (IN REF. 2).
                                       GHRL_BOVIN STANDARD; PRT; 116 AA.
09BDJ6; Q9GKY6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
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GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIM
N-OCTANOATE (BY SIMILARITY).
K -> E (IN REF. 2).
W; F55536DAC5FA59B6 CRC64;
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Pred. No. 0.0013;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
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SEQUENCE OF 24-99 FROM N.A.
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                                                                                                                                                                                                                                        Bos taurus (Bovine)
                                                                                                                                                                                       releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9913;
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                     GHRL_BOVIN
RESULT
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13 QAEGAEDELE 22

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V120_EBV
P03189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21996410; PubMed-12000953; BEDLINE-21996410; PubMed-12000953; BEDLINE-21996410; PubMed-12000953; BEDLINE-21996410; PubMed-12000953; BEDLINE-21996410; PubMed R.D., Cardeno-Tarraga A.-M., Chaillis G.L., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coelicolor A3(2).";
Nature 417:141-147(2002).
-!- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR THE SMALL NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Protease; Transcription regulation; Complete proteome.
DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                       18-FEB-2003 (Rel. 41, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small neutral protesse regulatory protein.
MPRR OR WRRA2 OR SCO7433 OR SC6D11.29.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomycese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 328
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Last annotation update)
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                                                                                                                              328 AA.
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100.0%; Pred. No. 4;
tive 0; Mismatches
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InterPro; IPR000847; HTH_LysR.
InterPro; IPR0005119; LysR_subst.
Pfam; PF00126; HTH_L1; 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
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32, Last seque
41, Last annoi
                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
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Les 7; Conservative
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                72
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                QAEGAEDELE
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28-FEB-2003
                                                                                                                    MPR2_STRCO
Q9L127;
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P43161;
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SEQUENCE
                  63
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ID MPRR_S
AC P43161
DT 01-NOV
DT 01-NOV
DT 28-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-921992468; Pubmed-1547948; Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O., Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O., McGinley M.O., Rohde M.F., Katzowitz J.L., Zukowski M.M.; McGinley M.O., Rohde M.F., Ratzowitz J.J., Zukowski M.M.; Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans."; Gene 111:125-130(1992).
-i- FUNCTION: TRANSCRIPIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE SMALL NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                           Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T.; "Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans 66 a novel neutral protease gene with an adjacent divergent putative regulatory gene."; Can. J. Microbiol. 38:912-920(1992).
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                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epstein-barr virus (strain B95-0) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000847; HTH_LysR.
InterPro; IPR005119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00466; LysR_substrate; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation: DNA_binding; Activator.
DNA_BIN 20 39 H-T-H MOTIF (POTENTIAL).
CONFLICT 270 270 G -> AR (IN REF. 2).
SEQUENCE 344 AA; 37415 MW; 485C82C813B52312 CRC64;
                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 7; DB 1;
100.0%; Pred. No. 4.2;
tive 0; Mismatches
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21-JUL-1986 (Rel. 01, Last sequence update)
10-CT-1996 (Rel. 34, Last annotation update)
Capsid assembly protein BOLFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1239 AA.
neutral protease regulatory protein
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EMBL; M89476; AAA26804.1; ALT_INIT.
                                                                                                                                                                                                                                                                                             STRAIN-66 / 1326;
MEDLINE-93099553; Pubmed-1464066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-305 FROM N.A.
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nes 7; Conservative
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                                                                  Streptomyces lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALAGWLR 110
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                                                                                                                                                                           NCBI_TaxID=1916;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                   SEQUENCE
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PROPEP
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                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                          "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-1; Synonyms-Chrelin;
IsoId-09BEF8-1; Sequence-Displayed;
Name-2; Synonyms-del-Ginl4-ghrelin;
IsoId-09BEF8-2; Sequence-VSP_003244;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                        TOGETHER HSV-1 UL37,
            Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomasetto C., Wendling C., Rio M.-C., Poltras P.; "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHRL_CANFA STANDARD; PRT; 117 AA.
Q9BEF8: Q9BEF7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
65-E10 precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
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                                                                                                                                                                                                                                                                                                                           30.4%; Score 7; DB 1; Length 1239; 100.0%; Pred. No. 13; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;
                                                                    Nature 310:207-211(1984).
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER H.
EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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MEDLINE-84270667; PubMed-6087149;
                                          Tuffnell P.S., Barrell B.G.;
                                                                                                                                                                                                                                                     EMBL; V01555; CAA24841.1; -.
                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 7; Conservative
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Capsid assembly.
                                                                                                                                                                                                                                                                                                                                                                                      14 AEGAEDE 20
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                                                                                                                                                                                                                                                                                                                             Query Match
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MEDLINE-91035433; PubMed-2229062;
Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
Negri A., Ronchi S.;
"The Ch21 protein, developmentally regulated in chick embryo, belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89261749; PubMed-2498647;
Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
"Rapid repression of quiescence-specific gene expression by epidermal growth factor, insulin, and pp60v-src.";
Mol. Cell. Biol. 9:1371-1375(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
MEDLINE-92147639; PubMed=1737754;
Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
Hayashi K., Quarto R., Cancedda R.;
"Expression, regulation, and tissue distribution of the Ch21 protein
during chicken embryogenesis.";
J. Biol. Chem. 267:2979-2985(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giannoni P., Dozin B., Zambotti A., Neri M., Cancedda R.; "Differentiation-dependent activation of the extracellular fatty acid binding protein (EXFABP) gene in chicken embryo chondrocytes."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
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EMBL; AJ298295; CAC29155.1; -.
EMBL; AJ298296; CAC29156.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR00544; Preproghrelin.
Pfam; PF04643; motilin_ghrelin.
Pfam; PF04644; motilin_ghrelin; 1.
Pranry; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
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P21766; P21928; O9PWN);
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Extracellular fatty acid binding protein precursor (Ex-FABP)
(Quiescence-specific protein) (P20K) (Ch21 protein).
                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
GHREIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SI
N-OCTANOATE (BY SIMILARITY).
MISSING (in lasform 2).
/FTIG-VSP_002244.
x; 3ES7FED9D1847CF7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6;
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100.08; Pre
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51
117
26
37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted
-!- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C., Camardella L., Negri A., Ronchi S.; "The maino terminal sequence of the developmentally regulated Ch21 protein shows homology with amino terminal sequences of low molecular weight proteins binding hydrophobic molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR FATTY ACID BINDING PROTEIN.
                                                                                                                                                                                                                        Nakano T., Graf T.; Identification of genes differentially expressed in two types of
superfamily of lipophilic molecule carrier proteins.";
.. Chem. 265:19060-19064(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PTM: Does not seem to be glycosylated.
-1- MISCELLANEOUS: Developmentally regulated in chick embryo.
-1- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                            Cancedda F.D., Malpell M., Gentili C., Di Marzo V., Bet P., Carlevaro M., Cermelli S., Cancedda R.; The developmentally regulated avian Ch21 lipocalin is an extracellular fatty acid-binding protein."; paiol. Chem. 271:20163-20169(1996).
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2 AND 4).
2 AND 4).
                                                                                                                                                Blochem. Blophys. Res. Commun. 168:933-938(1990)
                                                                                                                                                                                                                                                       v-myb-transformed avian myelomonocytic cells.";
Oncogene 7:527-534(1992).
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F -> S (IN REF.
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STRAIN-White leghorn; TISSUE-Bone marrow;
MEDLINE-92195690; PubMed-1549365;
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Interpro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; l.
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                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-20513977; Pubmed-11058755;
                                           SEQUENCE OF 21-48.
MEDLINE-90267487; Pubmed-2346493;
                                                                                                                                                                                                                                                                                                                  MEDLINE-96355330; PubMed-8702740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
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EMBL; X61199; -; NOT ANN
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-: FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine confident and glutamate. The hish subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hisf for the synthesis of IGP and AICAR (By similarity).
                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (ImGP synthase subunit hisH) (IMGP synthase subunit hisH) (IMGP synthase subunit hisH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ylamino)methylideneamino|-i-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)0.
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-1- SUBGNIT: Heterodimer of hisH and hisF (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promi, Proull, GATASE, I.
PROSITE: PSO0442; GATASE_TYPE_I; 1.
Histidine blosynthesis; Transferase; Glutamine amidotransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
                                                                         Length 178;
                                                                                                              Indels
 F -> S (IN REF. 1).
L -> V (IN REF. 1).
ODDBDC33C1A0C6B8 CRC64;
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. 26;
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SIMILARITY
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9
                                                                             Score 6;
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                                                                                                 Pred.
                                                            26.1%; Scu-
100.0%; Pred
0; F
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MEDLINE-98037514; PubMed-9371463;
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IPR000991; GATase_1.
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                                      20201 MW;
                                                                                                                Conservative
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62
96
178 AA;
                                                                                             Similarity
6; Conserv
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ACT_SITE 77
ACT_SITE 177
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027568;
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   CONFLICT
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21-JUL-1986 (Rel. 02, Last sequence update)
23-OCT-1986 (Rel. 02, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (ACTH); Melanotropin alpha (Alpha-MSH);
16-OCT-2001 (ACTH); Melanotropin alpha (Alpha-MSH);
16-OCT-2001 (ACTH); Melanotropin peta (Beta-MSH);
16-OCT-2001 (ACTH); Melanotropin beta (Beta-MSH);
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Gen K., Hirai T., Kato T., Kato Y.;
"Presence of the same transcript of pro-opiomelanocortin (POMC) genes
in the porcine anterior and intermediate pituitary lobes.";
Mol. Cell. Endocrinol. 103:101-108(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolleau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.; "Complete structure of the porcine pro-opiomelanocortin mRNA derived from the nucleotide sequence of cloned cDNA."; Nucleic Acids Res. 11:8063-8071(1983).
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S., Davis S.B., Eigner E.A., Shakespeare N.E.; "Studies with corticotropin. III. Determination of the structure of Deta-corticotropin and its active degradation products."; J. Am. Chem. Soc. 78:5067-5076(1956).
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-84239667; Pubmed-6547437;
Oates E., Herbert E.;
"5' sequence of porcine and rat pro-opiomelanocortin mRNA.
and two rat forms.";
            E8EFA43EC9163AEF CRC64;
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Riniker B., Steber P., Rittel W., Zuber H.;
Revised amino-acid sequences for porcine and human
adrenacorticotrophic hormone.
                                    DB 1;
                                                                                                                                                                   267 AA.
                                 26.1%; Score 6; DB ]
100.0%; Pred. No. 28;
tive 0; Mismatches
 BY SIMILARITY
                                                                                                                                                                   PRT;
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Nature New Biol. 235:114-115(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-84069823; PubMed-6196724;
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            21348 MW;
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                                                            Conservative
                                                                                                                                                                   STANDARD;
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179 1
198 AA;
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                                    Query Match
Best Local Similarity
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MEDILINE-F6100762; Pubmed-1207728;
MEDILINE-F6100762; Pubmed-1207728;
MORTIS H.R.;
MORTIS H.R.;
"Identification of two related pentapeptides from the brain with pobent opiate agonist activity.";
Nature 258:577-579(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acta Biochim. Biophys. Acad. Sci. Hung. 11:121-122(1976).
-1- FUNCTION: ACTH STIMULATES THE ADRENAL GLANDS TO RELEASE CORTISOL.
-1-- FUNCTION: MSH (MELANOCYTE-STIMULATING HORMONE) INCREASES THE
PIGMENTATION OF SKIN BY INCREASING MELANIN PRODUCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris J.I., Lerner A.B.; "Amino-acid sequence of the alpha-melanocyte-stimulating hormone."; Nature 179:1346-1347(1957).
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                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (In) Melenhofer J. (eds.);
Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.,
                                                                            'Re-examination of the sequence of the C-terminal tryptic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: ACTH AND MSH ARE PRODUCED BY THE PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilardeau C., Chretien M.; "Complete amino acid sequence of porcine beta-lipotropic hormone
                                                                                                                                                                                                           SEQUENCE OF 136-174.

MEDLINE=91071194; PubMed=2174774;

MEDLINE=91071194; PubMed=2174774;

Voigt K., Stegmaier W., McGregor G.P., Roesch H., Seliger H.;

"Isolation and full structural characterisation of six adrenocorticotropin-like peptides from porcine pituitary gland. Identification of three novel fragments of adrenocorticotropin two forms of a novel adrenocorticotropin-like peptide.";

Eur. J. Blochem. 194:225-236(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pankov Y.A., Yudaev N.A.;
"Complete amino acid sequence in the molecule of porcine beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris J.I., Roos P.; "Amino-acid sequence of a melanophore-stimulating peptide.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-71111231; PubMed-5543613; Cafef L., Barat E., Cseh G., Sajgo M.; Rafac acid sequence of porcine beta-lipotropic hormone."; Biochim. Biophys. Acta 229:276-278(1971).
                                                                                                           from porcine adrenocorticotropic hormone."; Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972)
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Geschwind I.I., Li C.H., Barnafi L.;
"The structure of the beta-melanocyte
MEDLINE-74306590; PubMed-4369114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISION TO 211.
MEDLINE-73048217; PubMed-4673865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS (LIPOTROPIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 178:90-90(1956).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 217-234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 136-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 177-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 237-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ann Arbor (1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MELANOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (beta-LPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glands.
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Embryo, Larva, and Pupae;
MEDLINE-84205681; PubMed-6202423;
Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
"Organization of contractile protein genes within the 88F subdivision
                                                                                                                                                                                                                                                                       CORTICOTROPIN.
MELANOTROPIN ALPHA.
CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
                                                                                                                                                                                                                                                                                                   LIPOTROPIN BETA.
LIPOTROPIN GAMMA.
MELANOTROPIN BETA.
BETA-ENDORPHIN.
MET-ENKEPHALIN.
AMIDATION (G-88 PROVIDE AMIDE GROUP).
AMIDATION (G-149 PROVIDE AMIDE GROUP).
N-LINKED (GLCNAC. . ) (POTENTIAL).
R -> T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
          PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD THE DIFFERENT ACTIVE PEPTIDES.
                                                                                                                                                                                                                   Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 267;
                                                                                                                                                                                                                                                                                                                                                                                              G -> S (IN REF. 3 AND 4).
T -> A (IN REF. 3 AND 4).
G -> E (IN REF. 3 AND 4).
A -> S (IN REF. 4).
A -> S (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPM2_DROME STANDARD; PRT; 284 AA. P09491; 024408; Q24408; Q24408; Q24408; Q8SZ65; Q9VF95; 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Tropomyosin 2 (Tropomyosin 1):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC).
                                                                                                                                                                                                                                                   NPP.
MELANOTROPIN GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                              -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%; Score 6;
                                                                                                                                                                                        PR001941; Mcortin_ACTH.
                     ACTIVE PEPTIDES
                                                                                                                                                                                              Pfam; PF00976; ACTH_domain; 1. PRINTS; PR00383; MELANOCORTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llarity 100.0%;
Conservative 0
                                                                                                                                   EMBL; X03561; CAA27248.1; -. EMBL; X00135; CAA24968.1; -.
                                                                                                                                                        EMBL; S73519; AAB32312.1; -. EMBL; K01879; AAA31104.1; -.
                                                                                                                                                                                                                               Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GAEDEL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 6; Conserv
                                                                                                                                                                             PIR; A93496; CTPGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAEDEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                        InterPro; ]
                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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PEPTIDE
PEPTIDE
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PEPTIDE
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Matches
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DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                              (PDCD1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLFNEKEKYKAICDDLDQTFAELTGY -> ELGINKDRYKS
                                                                                                                                      Name-Embryonic; Synonyms-129, A, B, e; Isold-p09491-2; Sequence-VSP_006616; DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY. SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY. CAUTION: Ref. 6 sequence differs from that shown due to erroneous
                    SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
MEDLINE-8215579; PubMed-4000944;
Boardman M., Basi G.S., Storti R.V.;
"Multiple polyadenylation sites in a Drosophila tropomyosin gene are used to generate functional mRRAs.";
Nucleic Acids Res. 13:1763-1776(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LADEMDSTFAELAGY (in isoform Embryonic).
- Tyrid-VSP-006616.
- Y (IN REF. 1).
- O - L (IN REF. 1).
- Y (IN REF. 1).
- R - D (IN REF. 1).
- R - D (IN REF. 1).
- R - D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-ocr-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Programmed cell death protein 1 precursor (Protein PD-1) (hPD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00326; TROPOMYOSIN; 1.
Muscle protein; Colled coil; Repeat; Alternative splicing; Multigene family.
VARSPLIC 259 284 RLFNEKEKYKAICDDLDQTFAELTGY ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                     Event=Alternative splicing; Named isoforms=2;
Name=Thoracic; Synonyms=127, t;
IsoId=P09491-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Score 6; DB 1.100.0%; Pred. No. 38; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                     EMBL; K02623; AAA28971.1; -:
EMBL; K02622; AAA28971.1; JOINED.
EMBL; K03277; AAA28973.1; -:
EMBL; K03277; AAA28973.1; -:
EMBL; K03277; AAA28973.1; -:
EMBL; X0220; AAA28973.1; -:
EMBL; X02220; AAA48709.1; -:
EMBL; X02220; CAA26142.1; ALT_SEQ.
PIR; A25624; A25624.
                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0004117; Tm2.
InterPro; PR000533; Tropomyosin.
Pfam; PF00261; Tropomyosin; I.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
PCD1_HUMAN STANDARD; PRT
AC 015116; 000517;
DT 01.NOV-1997 (Rel. 35, Created)
DT 16-0CT--2001 (Rel. 40, Last sequent)
DT 15-SEP-2003 (Rel. 42, Last annotes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 11 M
88 88 Q
95 25 I
255 255 R
284 AA; 32981 MW;
                                                                                                                                                                                                                                                                                                                             EMBL; K02622; AAA28970.1; -.
                                                                                                                                                                                                            gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 EDELEV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 EDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
-i- SIMILARITY: Contains I immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
SIGNAL 1 20 POTENTIAL.
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE-9747511; PubMed-9332365;
MEDILINE-9747511; PubMed-9332365;
Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
"The buman PD-1 gene: complete cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R., Burrows P.D., Billips L.D.;
Gene 203:253-253(1997).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                      MEDIINE-99154844; PubMed-7851902; Shinohara T., Taniwaki M., Ishida Y., Kawaich M., Honjo T.; "Structure and chromosomal localization of the human PD-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH OTHER FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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PROGRAMMED CELL DEATH PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Score 6; DB 1; Length 288; 100.0%; Pred. No. 39; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A5210AD50C3046C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L27440; AAC41700.1; -.
EMBL; U64863; AAC51773.1; -.
PIR; A55737, A55737.
HSSP; POIGO7; IREI
Genew; HGNC:8760; PDCD1.
MIM; 600244; -.
GO; GO:0004871; F:signal transducer activity; TAS.
GO; GO:0006915; P:apoptcosis; TAS.
GO; GO:0006515; P:development; TAS.
GO; GO:0006515; P:development; TAS.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-light.
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-> S (IN REF 1)
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                                                                                                                                                                                                                             Genomics 23:704-706(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 6; Conserv
                                                   NCBI_TaxID=9606;
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CYTOPLASMIC (POTENTIAL).

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PARB_HELPJ
                                                    CARBOHYD
NON_TER
                  DISULFID
                                                                                        SEQUENCE
                                     BINDING
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 DOMAIN
                                                                                                                                                                                                                                                                                             RESULT 13
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 FFFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular evolution of the cottoid fish endemic to Lake Baikal
deduced from nuclear DNA evidence.";
Mol. Phylogenet. Evol. 8:415-422(1997).

**Holylogenet. Evol. 8:415-422(1997).

**Holylogenet. Evol. 8:415-422(1997).

**INTED TO CIS.RETINAL.

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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actihopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Abyssocottidae; Limnocottus.
                                                                                                                                                                                                                                                                                                                                                                                                                  Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                          289 AA
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                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98086781; PubMed-9417898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U97271; AAB61725.1; -.
HSSP; P02699; 1BOJ.
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
Rhodopsin (Fragment).
                                                                                                                                                                                                                                                    Limnocottus pallidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPSIN SUBFAMILY.
                                 277 LRPEDG 282
6 LRPEDG 11
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=61634;
                                                                                                                          OPSD_LIMPA
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AEDLINE-99120557; PubMed-9923682;
ALD R.A. Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Tumbison R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID-85963;
                                                                                          RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                              32715 MW; 160D08E17E5E1280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable chromosome partitioning protein parB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 AA.
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                                               BY SIMILARITY
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InterPro; IPR004437; ParB_part.
InterPro; IPR003115; ParBc.
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    >289
158
267
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281 >2
81 267
267
171 172
289 AA;
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245 AEDELE 250
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-I- FUNCTION: Part of an ATP-driven transport system for a metal; this protein has affinity for Zn(II), Fe(III) and Cu(II).
-I- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the bacterial solute-binding protein family 9. Lipoprotein receptor antigen (Lral) subfamily.
                                                                                                                                                                                            Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                             28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Metal Age transporter substrate-binding lipoprotein precursor.
MTSA OR SPYMI8_0494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTSA_STRPY STANDARD; PRT; 310 AA.
09A157; 09RN17; 09RNJ0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Metal ABC transporter substrate-binding lipoprotein precursor.
MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL ABC TRANSPORTER SUBSTRATE-BINDING LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0690; ADHESNFAMILY.
PROSITE; PSO0013; PROKAR_LIPODROTEIN; 1.
Transport; Zinc transport; Iron transport; Copper; Membrane; Lipoprotein; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-ACYL DIGLYCERIDE (PROBABLE), 40F613659AAD1768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                             Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
           310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.1%; Score 6; DB 1
100.0%; Pred. No. 41;
iive 0; Mismatches
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Interpro; IPR006127; SBP_bac_9.
Pfam; PF01297; SBP_bac_9; 1.
          PRT;
                                                                                                                                                                    STRAIN-MGAS8232 / Serotype M18;
MEDLINE-21927593; Pubmed-11917108;
                                  (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE009988; AAL97215.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34330 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 AA;
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                                                                                                                                 NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 EDGGQA 14
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                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                      Streptococcus
                                 28-FEB-2003
       MTSA_STRP8
Q8P280;
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                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SF370 ATCZ 700294 / Serotype M1;
MEDLINE-21192684: PubMed=11296296;
MEDLINE-21192684: PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. SCI. U.S.A. 98:4658-4663(2001).
                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
STRAIN-SF370 / ATCC 700294 / Serotype M1, and AP1 / Serotype M1;
MEDIINE-20032372; Pubmed-10564500;
Janulczyk K., Pallon J., Bjoerck L.,
Indentification and characterization of a Streptococcus pyogenes ABC transporter with multiple specificity for metal cations.";
Mol. Microbiol. 34:596-606(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-MGGA315 / Serotype M3;
MEDLINE-2133808; Pubmed-1212206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlisvert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
BETAL ABCTAL ABCATER SUBSTRATE-BINDING LIPOPROTEIN.
N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0690; ADHESNEAMILY.
PROSTIE; PS001013; PROKAR_LIPOPROPEIN; 1.
Transport; Zinc transport; Iron transport; Copper; Membrane;
Lipoprotein; Signal; Complete protecome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP005145; BAC64634.1; ALT_INIT
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InterPro, IPR006128; Lipoprotein_4.
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Streptococcus.
NCBI_TaxID=1314, 198466;
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FT CONFLICT 26 26 T -> A (IN REF. 1).

FT CONFLICT 44 44 A -> E (IN REF. 1).

FT CONFLICT 49 50 A -> CG (IN REF. 1).

FT CONFLICT 49 50 A -> VM (IN REF. 1).

SQ SEQUENCE 310 AA; 34358 MW; BOF829EFIC72CADC CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 41;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 EDGGQA 14

| | | | | | |
| Db 94 EDGGQA 99

Search completed: September 11, 2003, 17:52:41
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087801 pseudomonas Q86705 bifldobacte Q65548 bovine herp Q4180 homo saplen Q91403 bitldobacte Q8180 homo saplen Q91403 bitldopace Q8140 homo saplen Q92502 onchocerca Q8459 onchocerca Q8459 onchocerca Q8457 onchocerca Q8597 accharomyc Q91447 onchocerca Q0567 accharomyc Q9504 homo saplen Q9574 homo saplen Q91404 organ satur Q9113 zymomonas m Q8xxy cralstonia s Q8xxy cralstonia s Q8xxy cralstonia s Q8500 vibrio chol Q8169 vibrio chol Q8169 acanthochel Q95014 lactobacill Q98115 lactobacill Q98115 lactobacill Q98117 lactobaci
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 20; DB 4; Length 117; 100.0%; Pred. No. 2.4e-13; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025791; AAH25791.1; -.
InterPro; IPR006737; mctilln_assoc.
InterPro; IPR006738; mctilln_abrelin.
Pfam; PF04643; mctilln_assoc; 1.
Pfam; PF04644; mctilln_abrelin; 1.
SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;
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Last annotation update)
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Q65548
Q43180
Q8JFY6
Q8N8H9
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Q8ZBU1
Q25622
Q8WT59
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Q25619
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Q8WT56
Q8WT57
Q05697
Q8N9A4
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QBCH53;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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TISSUE-Blood;
 Ghrelin.
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Matches
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Q8CH53
ID Q8CH9
AC Q8CH9
DT 01-M
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Q8ch53 meriones un
Q92x7 arabidopsis
Q817e4 arabidopsis
Q81063 streptomyce
Q8vp52 streptomyce
Q8vp52 streptomyce
Q8vy49 ralstonia s
Q9135 pseudomonas
Q95470 drosophila
Q966v1 drosophila
Q85z1 pyrobaculum
Q8zz1 pyrobaculum
Q8zz1 pyrobaculum
Q8zy185 onchocerca
Q8bbn4 xanthomonas
                                                                                        September 11, 2003, 17:46:02; Search time 22.016 Seconds (without alignments) 269.586 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                   OM protein - protein search, using sw model
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Q8CH53
Q8Z47
Q8L7E4
Q65529
Q9L063
Q8VP52
Q8CNY4
Q8XX49
Q9XX49
Q9XX49
Q9XX50
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Q8ZZR1
P91785
Q8PBN4
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Gapop 60.0 , Gapext 60.0
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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sp_rodent:*
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Match Length DB
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23
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Last sequence update) Last annotation update)

Created) PRT;

433 AA

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                             (TrEMBLrel. 22, (TrEMBLrel. 22, 1 (TrEMBLrel. 23, 1
  PRELIMINARY;
                                                                       Hypothetical protein. AT4G32720.
                                                                                                                                                           NCBI_TaxID=3702;
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              08L7E4;
01-OCT-2002 (
01-OCT-2002 (
01-MAR-2003 (
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Best Local Si
Matches 8;
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065529;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamilya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyem M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                           Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
Ishii H.;
                                                                                                                                                         "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF442491; AA006655.1; -
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                            Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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                                                                                                                                                                                                                                 Length 117;
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                                                                                                                                                                                                                              47.8%; Score 11; DB 11; Length 11
100.0%; Pred. No. 0.00062;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY056237; AAL07086.1; -. InterPro; IPR00634; Lupus_La. InterPro; IPR006630; Lupus_La_dom. InterPro; IPR006630; Lupus_La_dom. InterPro; IPR00664; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Full Length cDNA of gene AT4g32720 (GI:7270219).";
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                                                                                                                                                                                                                                                                                                                                                                                          433
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                                                             Local Similarity 100.
hes 11; Conservative
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                                                                                                                                                                                                                                                                                      12 GQAEGAEDELE 22
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM;
SEQUENCE 433 AA; 480
                 Ghrelin preproprotein.
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Best Local Similarity
Matches 8; Conserv
                                                                                                               SEQUENCE FROM N.A.
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                                                                                   NCBI_TaxID=10047;
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Matches
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SEQUENCE FROM N.A.
SOUTHWICK A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. BMBL, AY136302, AM96968 1; --InterPro; IPR002344; Lupus_La.
InterPro; IPR005344; Lupus_La.
InterPro; IPR006530; Lupus_La.
InterPro; IPR000504; RNA_rec_mot.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 54.1 kDa protein.
F4DII.80 OR AT4G32720.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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SEQUENCE 433 AA; 48126 MW; CFFF611A29AA0318 CRC64;
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100.0%; Pred. No. 2.8;
tive 0; Mismatches
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
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nes 8; Conserv
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313 AA

PRT;

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PRELIMINARY;
                                                                                                                                                                                                                                                                                                             STRAIN=C5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                       Q8VP52
                             Q8VP52
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SEQUENCE FROM N.A.
Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETRAIN-3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coellcolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Bacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.4%; Score 7; DB 16; Length 103; 100.0%; Pred. No. 8.5; 1.1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.8%; Score 8; DB 10; Length 483; Best Local Similarity 100.0%; Pred. No. 3.1; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR.2000) to the EMBL/Genbank/DDBJ databases.
EMBL; ALO2237; CAA185991; ...
INTERPIC; IPR002344; Lupus_La.
InterPro; IPR00530; Lupus_La.
InterPro; IPR005630; Lupus_La.
InterPro; IPR00564; RNA_rec_mot.
Pfam; PF00076; rrm; I.
                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417:141-147(2002).
EMBL. AL939114; CAB87228.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10639 WW; 9316F1F38C1BD492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 483 AA, 54125 MW; 20840B34A0BC94E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09L063;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO2791.
SCO2791 OR SCC105.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                           PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50102; RRM; 1.
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302 QAEGAEDE 309
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DGGQAEG 54
                                                                                                                       SEQUENCE FROM N.A.
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Q9L063
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                Desanti C.L., Strohl W.R.;
"Characterization of the Streptomyces sp. strain C5 snp locus and development of an snp-derived expression vector family.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
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0
                                                                             LysR-like transcriptional activator SnpR.
Streptomyces sp. C5.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE016748; AAO04949.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY072041; AAL61992.1; -.
InterPro: IPR000847; HTH_LysR.
InterPro: IPR001947; HTH_LysR.
InterPro: IPR05119; LysR_subst..
Pfam; PF00126; HTH_1: 1.
Pfam; PF00126; HTH_LYSR.
PRINTS: PR00039; HTH_LYSR.
PROSITE; PS00044; HTH_LYSR.
PROSITE; PS00044; HTH_LYSR.
DNA-binding; Transcription; Transcription.
SEQUENCE 313 AA; 34258 MW; C907C8AF5IC3FA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 AA; 48732 MW; FF2490AD097F437D CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trigger factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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100.0%; Pred. No. 23;
Live 0; Mismatches
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Matches 7; Conservative
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Matches 7; Conservative
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180 DGGQAEG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-ATCC 12228;
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                                                                                                                                                                            NCBI_TaxID=45212;
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Q8XY49
ID Q8XY
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910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;

Complete proteome. SEQUENCE 910 AA;

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STRAIN-ATCC 15692 / PAO1;

MEDLINE-2043737; Pubmed-10984043;

Stover C.K., Pham X.-O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L. Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnec S., Demange N., Gaspin C., Lavie M., Molsan A., Robert C., Saurin W., Schiex T., Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
BMBL: AL646067: CAD15616.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                     Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 887;
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                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                         probable phage-related tail transmembrane protein parts of RSC1914 OR RSC3483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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ProDom; PD00511; Aconitase_N; 1.
TIGRAMS; TIGR01341; Aconitase_1; 1.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-GMI1000;
MEDLINE-21681879; Pubmed-11823852;
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Interpro; IPR001573; Aconitase C.
Interpro; IPR001030; Aconitase C.
Pfam; PF00330; aconitase; 1.
Pfam; PF00694; Aconitase C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004584; AAG04951.1; -.
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01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                   (TrEMBLrel. 20, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                   Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.4 Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aconitate hydratase 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE 887 AA
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
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                                   01-MAR-2002
01-MAR-2002
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Q913F5
ACCOORDING TO THE PROPERTY OF 
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hostins R.A., Galle R.E.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarogul L., Beasley E.M.,
Ballew R.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis N.C., Busam D.A., Bultler H., Cadieu E., Center A., Chadra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Choron K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Clodek A., Gong F. Gorrell J.H., Ray J., Wel M.-H., Ibegvam C.,
RA Hostin D., Houston K.A., Howland T.J., Herrandez J.R., Hork M. A.
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia Z.,
Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lux, Matteri B., Morfntcsh T.C., McLeado J.M., Nethorson D.,
Retulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.
Relazzolo M., Pittuman G.S., Pan S., Pollard J., Puri V., Wengere M. Spier E., Spradling A.C., Stapleton M., Stuong K., Sunth Y., Saler E., Spradling A.C., Stapleton M., Stuong G.N., Santh R.,
Spier E., Spradling A.C., Stapleton M., Stuong G., Zheo Q., Zhen Wang Z.-Y., Wassarman D.A., Wellsenbach J.,
Wang Z.-Y., Wassarman D.A., Wellsenbach J.,
Walliams S.M., Woodege T., Worley C., Well W., Santh M.,
Sleiner K., Zhong F.N., Zhong W.,
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                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                 GG18408 protein.
REXIN OR CG3451 OR CG18408 OR CG18409.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                   Length 910;
                                                                  Indels
                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                        DB 16;
      30.4%; Scor.
100.0%; Pred. No. cc.
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Ouery Match
Best Local Similarity الاست
ابع 7; Conservative
                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                          1 ALAGWLR 7
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us-09-853-253-5.oli.rspt

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-1- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
EMBL; AB053478; BAB62017.1; -.
                                FlyBase; FBgn0033504; rexin.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                        13 QAEGAED 19
                                                                                                                                                                                                                                                                                     37 QAEGAED 43
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                                                                                                                                                      SH3 domain.
                                                                                                                                                                    SEQUENCE
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Q8ZZR1
ID Q8ZZR1
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Yamzaki H., Willert K., Fish M., Nusse R.;
"Drosophila Rexin, a Novel SH3 Adaptor Protein of Axin and Arrow that is Essential for Living in Late Stage Embryo.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                          Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Wungall C.J., Lewis S.E., Shomitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Fertera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy W., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeilfer B., Stapleton M., Strong R., Striskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Drosophila melanogaster (Fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.4%; Score 7; DB 5; Length 2376; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2376 AA; 267666 MW; A5F2D0589BBB695C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003830; AAF58816.2; -. FlyBase; FBGn0033504; rexin. InterPro; PR00452; SH3. PR10FS; PR00452; SH3. PR0DOM; PD000066; SH3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamazaki H.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 100.
Matches 7; Conservative
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PROSITE; PS50002; SH3;
SEQUENCE 2376 AA; 2
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37 QAEGAED 43
                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 21173698; PubMed=11259647;

MIGHINE-21173698; PubMed=11259647;

A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potcock I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Bly B.,

A Rolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

R. Complete genome sequence of caulobacter creacentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

- I- SUMCLALDIAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

R. EMBL; AEGO09303, AAK24591.1; -.

R. HSSP; P15277: IMJC.
                                                                                                                                                                                                                                                                                                  Gaps
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SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09A542 PRELIMINARY; PRT; 69 AA. 09A542; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) cold-shock domain family protein.
                                                                                                                                                                                                                                30.4%; Score 7; DB 5; Len
100.0%; Pred. No. 1.4e+02;
:1ve 0; Mismatches 0;
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Pfam; PF00313; CSD; 1.
PRINTS; PR000050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
Pfam; PF00018; SH3; 3.

PRINTS; PR01217; PRCHEXTENSN.
ProDom; PD000066; SH3; 3.

SMART; SM00326; SH3; 3.

PROSITE; PS50002; SH3; 3.
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Matches 7; Conservative
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Matches 6; Conservative
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MEDINE-94336252; PubMed-8058358;
Trenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
Bradley J.E.;
"Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
antigens in microfiladermia positive individuals from Esmeraldas
Province, Ecuador.";
Parasite Immunol. 16:201-209(1994).
BMBL: S71371; AAC60510.2; -.
NON_TER 98 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller J.H.;
"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
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P91785;
P91785;
D1-MAY-1997 (TrEMBLrel. 03, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Antigen maltose binding protein (Fragment).
Antigen waltose binding protein (Fragment).
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerciae.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                                                                    Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteacea;
Thermoproteaceac; Pyrobaculum.
NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL, AE009752; AAL62578.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 9492 MW; 22091651B45CADDI CRC64;
   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE0124.
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100.0%; Pred. No. 90;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
Pubmed-11792869;
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 6; Conservative
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45 ALAGWL 50
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51 LRPEDG 56
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Human signal pepti Human polypeptide Human sign3 polyp Zsign3 protein. H Human ghrelin prep Amino acid sequenc Human sign3 prote Human Ro polypept Human secreted/rra Novel human secreted and Novel human secreted/rra Human secreted/rra Human secreted/rra Human secreted/rra Human secreted/rra Human propepti Human propepti Human propepti Human propepti Human PRO polypept Human PRO polypepti Human PRO polypepti

Title: Perfect score:

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Sequence:

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Searched:

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Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
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                     AAB62649
AAB20101
AAB60511
                                                     ABB78319
AAE23838
AAE15883
ABU66790
ABU67066
ABU59871
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ABU58046
ABU58977
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AAY66708
AAU12392
AAB65231
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AAB60510
AAB60521
AAB60520
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ABP58240
AAR98903
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ABU59420
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ABU13937
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ABP08975
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 10-MAY-2001; 2001US-0853253
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JS2002055156-A1
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AAE23840;
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 Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human csig33-linke
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Human des Glinke
                                                                     September 11, 2003, 17:21:03; Search time 23.984 Seconds (without alignments) 152.215 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                       fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                  1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE15885
AAE15886
AAE23839
AAE23839
AAE33810
AAE33810
AAB60517
                                                     OM protein - protein search, using sw model
                                                                                                                                           1 ALAGWLRPEDGGQAEGAEDELEV
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Human polypeptide
Human ORFX protein
Rat des-Gin14-ghre
Rat ghrelin prepro
Porcine ghrelin pr
Bovine ghrelin pr
Svenopus laevis nuc
Murine APLP1. Mus

Human colon cancer Novel human diagno Novel human diagno Drosophila melanog

Deisher TA, Bishop PD;

Jaspers SR, Sheppard PO,

WPI; 2002-443750/47

(JASP/) JASPERS S R. (SHEP/) SHEPPARD P O. (DEIS/) DEISHER T A.

Score

è. Result

12222222

(BISH/) BISHOP P D.

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uncleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The sequences of the invention and their complements are used as probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in amples (e.g. by enzyme linked immunosorbent assay (ELSA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. ZSIG33-like peptide. Is used in protein therapy. The present sequence is human zsig33-like peptide. ZSIG33-linker peptide.
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                <code>ZSIG33-Like</code> peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
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                                                                                                                                       The invention relates to zsig33-like peptides and their corresponding
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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100.0%; Pred. No. 3.6e-11;
tive 0; Mismatches 0;
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                                                                                                 Claim 1; Page 28; 34pp; English.
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Best Local Similarity 100.
Matches 23; Conservative
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DEISHER T A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AA;
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AAE23841
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The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones.

The sequences of the invention and their complements are used as treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic against contractility in the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and hormones, and/or hormones in the panceas. zsig33-like DNA is used in gene therapy and zsig33-like peptide, zsig33-linker peptide.
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contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
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                                                      Claim 1; Page 28; 34pp;
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N-PSDB; AAD25760.
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23 AA;
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                                             Jaspers SR,
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Region
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                                                                caignal linker, zaignal beta, zaignal gamma, zaignal dalta and zaignal linker, zaignal beta, zaignal gamma, zaignal dalta and zaignal linker, zaignal beta, zaignama, zaignal dalta and zaignal linker, zaignal beta, zaignama, zaignal dalta and zaignal linker peptides and nucleic acid molecules encoding such zaignal linke peptides. zaignal peptides activate the immunocompromised in boosting immunocompromised patients such as human immunodefictency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and consistent in receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption chhancers for oral drugs which require fast nutrient action and to chance for oral drugs which require fast nutrient action and to attimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation of tissues associated for the expansion, differentiation of tissues associated with contractile tissues or to suppress or enhance contractility in vivo and to treat contractility in discrete with gastrointestinal contractility, secretion of diseases, zaside peptides and acids, secretion of hormone and acids, secretion of hormone as in the pancreas and/or branch.
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                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker
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                                                         invention relates to zsig33-like peptides (ZS33LP) including
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 23;
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                           Claim 1b; Page 81; 89pp; English.
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zsig33-like peptides -
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nes 23; Conserv
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Modified-site
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rice inversion paperides and nucleic acid molecules encoding such zaig33-tinker, zaig33-epsilon peptides and nucleic acid molecules encoding such zaig33-epsilon peptides and nucleic acid molecules encoding such zaig33-tinker peptides acitivate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodefictency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and captient receptors involved in growth regulation in the liver; blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption chhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and cortinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS31rp peptides, nucleic acids and/or antibodles are useful for treating discretes and and/or brains.

Contractility in vivo and contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                         New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene therapy. The present sequence is human zsig33-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to zsig33-like peptides (ZS33LP) including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                          Deisher TA, Bishop PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1c; Page 82; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2002 (first entry)
                                                                                          Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
(ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   zsig33-like peptides
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Homo sapiens
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                                                                           Region
                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to zaig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention and their complements are used as treatment of diseases associated with inappropriate 2siG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify and antigonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assays (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and azig33-like poptide. Zsig33-like peptide.
                                                                                                                                                                                                                                                                                                                                                                    251G33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; zsig33-like peptide; ZS33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33-linker peptide.
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                                                                                                                                                                                                                                                                             Deisher TA, Bishop PD;
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100.0%; Pred. No. 3.8e-11;
/note= "Hydrophilic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE15884 standard; peptide; 24
                                                                                                            10-MAY-2001; 2001US-0853253
                                                                                                                                              11-MAY-2000; 2000US-203300P
                                                                                                                                                                                                                                                                           Jaspers SR, Sheppard PO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                (JASP/) JASPERS S R. (SHEP/) SHEPPARD P O.
                                                                                                                                                                                                   (SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                                                                                                                           WPI; 2002-443750/47.
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Best Local Similarity
Matches 23; Conserva
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                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD38239
                                                                          09-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                  nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                               New polypeptides, useful for modulating gastric contractility, nu uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises
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                  /note= "Hydrophilic antigenic site"
7.18
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100.0%; Pred. No. 3.8e-11;
ive 0; Mismatches 0;
                                                              "Hydrophilic region
Location/Qualifiers 5..22
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                                                                                                                                                        10-MAY-2001; 2001WO-US15091
                                                                                                                                                                                       11-MAY-2000; 2000US-0569271
                                                                                                                                                                                                                                                     Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                               zsig33-like peptides
                                                                                                                                                                                                                                                                                 WPI; 2002-082982/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AA;
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                                                                                          WO200187933-A2
                                                                                                                         22-NOV-2001.
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Fri

Homo sapiens.

14-NOV-2002

Chopin LK,

02-APR-2003

Ghrelin;

breast;

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghreal in monologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by vectors and host cells comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptides. The peptides of the invention; and an assay and kit for detecting the peptides. The peptides caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth commone deficiency. The compounds of the invention are safe with commone deficiency. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                        New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 116;
                                                                                                                                                                                                                                                                Hosoda H, Matsuo H, Minamitake Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 121; DB 22;
100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0;
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24..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 186-187; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ALAGWLRPEDGGQAEGAEDELEV 73
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                                                                                                                                                                                                                                                                                                                                                                                                                   of infant growth disorders -
                                                                                                                                                     99JP-0338841.
                                                                                                                                                                          26-APR-2000; 2000JP-0126623
                                                                                      24-JUL-2000; 2000WO-JP04907
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nes 23; Conservative
                                                                                                                                                                                                                                                                Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                           WPI; 2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA;
                                                                                                                                                                                                                     (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF59647
  WO200107475-A1
                                                                                                                                 3-JUL-1999;
                                                                                                                                                     39-NOV-1999;
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                                             01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                     ; preproghrelin; GHS-R lb; benign prostatic hyperplasia; therapy; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, and exon-3 deleted preproghelin and/or a GHS-H lb proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghrelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choricorarchioma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herington AC;
                                                                                                                            Human exon 3-deleted ghrelin protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 34; 50pp; English.
AAE33410 standard; Protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2001; 2001AU-0004919.
17-DEC-2001; 2001AU-0009567.
                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2002; 2002WO-AU00582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001 (first entry)
                                                                                   (first entry)
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jeffery PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-111957/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD50726
                                                                                                                                                                                                                                                                                                      WO200290387-A1.
                                                                                                                                                                                                                  cancer; human.
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Homo sapiens

AAB60517;

RESULT

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Sequence Query Match

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Gaps

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Lal P, Tang Akerblom IE,
                          25-JUN-1999;
                                                                   31-JUL-1998;
                                                                                           11-DEC-1998;
                                                    26-JUN-1998
                                                                              01-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
06-JAN-2000
                                                                                                                                                                         Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM38890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM38890
ID AAM3
XX
AC AAM3
XX
DT 22-0
DY 22-0
XX
Huma
XX
KW Huma
KW Perli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                     The present sequence represents a protein designated Zaig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or alielite variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive conzymes, gastrointestinal motility, recruitment of digestive ansymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation Zaig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety cort treat obesity and other metabolic disorders where neurological elebation of the metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zigi3 agonists, antagonists and ligands and to produce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antisthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia; asthma; Crohn's disease; infection; Alzheimer's disease; schbrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                               Human polypeptide having homology to motilin, zsig33 - useful e.g.
                                                                                                                                                                                                                           to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 121; DB 20;
100.0%; Pred. No. 2.2e-10;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY87236 standard; Protein; 117 AA.
                                                                            97US-0822897.
                                                 98WO-US05620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
The 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                               Sheppard PO;
                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                       WPI; 1999-070071/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscular dystrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
                                                                                                                                                                                     N-PSDB; AAX04550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200000610-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                             24-MAR-1997;
24-MAR-1997;
WO9842840-A1
                                                   23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2000
                                                                                                                                               Delsher TA,
                        01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY87236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
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AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPBs have anticancer, anti-inflammatory, antimarcobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiaethmatic activities, and can be used in game therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Such diseases include cell proliferation (HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (Including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cathma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, Alzhaimer's, Parkinson's or Huntington's uncleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise specific antibodies (Ab) and to screen for genetic variations, and for chromosomal mapping, HSPP are also used to raise specific acids can be used for chromosomal mapping, HSPP are also used to raise specific acids can be used for chromosomal mapping, HSPP are also used to raise specific for admits and the screen for genetic variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                          Baughn MR;
k, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Gorgone GA, Corley NC, Guegler KJ, Bar
n IE, Au-Young J, Yue H, Patterson C, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 168-169; 327pp; English.
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99WO-US14484.
                                                                                 98US-0090762.
98US-0094983.
                                                                                                                                                                      98US-0102686.
98US-0112129.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-160673/14.
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Fri

Homo sapiens

leukaemia.

26-JUL-2001

19-JUL-2000; 03-AUG-2000; 14-SEP-2000; 19-OCT-2000;

09-JUL-2000; 21-JAN-2000; 25-APR-2000;

29-NOV-2000;

Tang YT, Zhao QA,

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skeletal dysplasis, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zsig33 polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of forming a reversible peptide-
receptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (comprising residues 24-7)
of AAB62649), where the receptor binds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
transduction in a dell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of disestive and
pancreatic enzymes and hormones, secretion of insulinilke growth factor-
1, secretion of non-zsig33 proteins. It is useful for modulating growth
hormone secretion in a mammal having a disease associated with abnormal
levels of growth hormone, such as osteoporosis, bone repair, bone
remodeling, low osteoblast levels, cartilage repair and remodeling,
zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-I; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; G-protein coupled receptor.
                                                                                                                                                                                                     24..37
/note= "specifically claimed fragment that binds to
the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 121; DB 22;
1larity 100.0%; Pred. No. 2.2e-10;
Conservative 0; Mismatches 0;
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 93-94; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.
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                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US32074.
                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0166765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-355879/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF83678
                                                                                                                                                                                                                                                                                               W0200138355-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-2000;
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                          31-MAY-2001
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                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, manunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinianian activity, chemoctactic/chemokinetic activity, haemoctactic and therapy, drug screening, as assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 121; DB 22;
100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as central nervous system injuries
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2000US-0552317
2000US-059042.
2000US-063450.
2000US-063450.
2000US-063450.
2000US-063450.
                                                                                                                                                                                                                          26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442253/47.
N-PSDB; AAI58046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.N.S disorders
                                                                                                                                       WO200153312-A1
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specification

Sequence

Query Match

AAB62649;

AAB62649
ID AAB6
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AC AAB6
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RESULT 12

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Gaps

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion conforming in calls. The peptides are ghreal in monologues and are concentration in cells. The peptides are ghreal in monologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides. The peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a giventh hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                           Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hosoda H, Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human zsig33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 182; 210pp; Japanese.
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                                                                                                                                                                                                                                                                                                                   23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of infant growth disorders -
                                                                                                                                                                                                                                                                       24-JUL-2000; 2000WO-JP04907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-159704/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                    (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF59645
                                                                                                                                                                      WO200107475-A1
                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the small intestine and pancreas. A novel peptide fragment of zsig33 termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insullin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum issue,
                                                                                              SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying
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/label- SGIP_peptide
/note= "this peptide is claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 121; DB 22;
100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                           /label Signal_peptide
24..117
                                                                                                                                                                                                                                                                                                                                       /label- Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US18306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0345157.
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  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-123010/13.
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                                                                                                                                           therapy; human.
                                               2sig33 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200100830-A1
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1999;
23-APR-2001
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AAB60511
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Length 117;
                              Indels
                                                                                                                                                                                                                                                                                              Short gastrointestinal peptide; SGIP; zsig33; motilin.
100.0%; Score 121; DB 22; 100.0%; Pred. No. 2.2e-10;
                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents human zsig33. The specification describes a short gastroinestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP SGIP may also be used as an antigon in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies against some the presence of SGIP in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                              New Short Gastrointestinal Peptide, which has homology to motilin, assetul for preventing, diagnosing and treating gastrointestinal disorders
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                                                                                                                                                                                                                                                                Delsher TA, Bishop PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Columns 39-40; 23pp; English.
               1..23
/mote= "signal peptide"
24..119
/mote= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                              30-JUN-2000; 2000US-0608810.
                                                                                                                                                                                               99US-141592P.
                                                                                                                                                                                                                                                                Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                             WPI; 2002-634794/68.
N-PSDB; ABV72214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 117 AA;
                                                                                                                                                                                             30-JUN-1999;
                                                                                             US6420521-B1
                                                                                                                             16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                disorders
 Key
Peptide
                                                Protein
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Search completed: September 11, 2003, 17:25:03 Job time : 24.984 secs

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24838, A 21437, A 4, Appli App11

Sequence 12, App. Sequence 12, App. Sequence 9, App. Sequence 24838, Sequence 21437, Sequence 27419, 1 Sequence 27950, 1 Sequence 2, App. Sequence 2, App. Sequence 6, App. Sequence 7, App. Sequence 7, App. Sequence 8, App. Sequence 8, App. Sequence 12553, App. Sequence 25523, App. Sequence 25523,

Sequence:

Run on:

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US-09-252-991A-20326
US-08-482-304-12
US-08-482-304-12
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US-09-252-991A-21437
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US-09-252-991A-27419
US-09-252-991A-27419
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US-08-252-991A-2468-0
US-09-341-4468-6
US-09-341-4468-6
US-09-341-4468-6
US-09-341-4468-6
US-09-341-4468-6
US-09-341-4468-6
                                                                                                                                                                                                              US-09-252-991A-25523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
PRIOR ADDITATE:
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09046479;
Patent No. 6291653;
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Saavislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                  2: ZymoGenetics, Inc.
1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                    US-09-046-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
 CITY:
STATE:
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 268, App
Sequence 17758, App
Sequence 17, Appl
Sequence 16, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Appl
Sequence 23604, A
Sequence 23606, A
Sequence 27327, A
Sequence 19723, A
Sequence 25921, A
Sequence 18853, A
Sequence 18853, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Appli
1, Appli
2, Appli
                                                                                  September 11, 2003, 17:21:03; Search time 6.14973 Seconds (without alignments) 158.243 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-608-B10A-4
US-09-996-243-268
US-09-996-243-268
US-08-339-152A-17
US-08-339-152A-16
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US-09-252-991A-27327
US-09-252-991A-19233
US-09-252-991A-19233
US-09-252-991A-18853
US-09-252-991A-18853
US-09-252-991A-18853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-521-220-1
-08-704-711A-2
                                                                                                                                                                                                                        328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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1 ALAGWLRPEDGGQAEGAEDELEV
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                     US-09-853-253-5
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Perfect score:
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Result

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Gaps

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Length 117; Indels

Query Match 100.0%; Score 121; DB 3; Best Local Similarity 100.0%; Pred. No. 6e-11; Matches . 23; Conservative 0; Mismatches 0;

MOLECULE TYPE: protein FRAGMENT TYPE: internal

ce 2, Appli

App11

Sequence Sequence Sequence Sequence

09-211-704A-9

Sequence 1, Appli Sequence 18600, A Sequence 4, Appli

JS-09-252-991A-18600

PCT-US94-08449A-4

Sequence

linear

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION UNBER: US/09/996,243
CURRENT FILING DATE: 2001-11.14
PRIOR APPLICATION NUMBER: 60/049787
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                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 121; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels (
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR FILING DATE: 1999-06-30
NUMBER OF SED ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILLING DATE: 1997-06-16
PRIOR PELICATION NUMBER: 60/062250
PRIOR PILLING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/065186
PRIOR PELICATION NUMBER: 60/065187
PRIOR PELICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILLING DATE: 1997-11-24
PRIOR PILLING DATE: 1998-10-24
                                                                                                                                                                                                                                                                                                                                                                                                           52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEV 23
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APPLICATION NUMBER: 60/083322
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                  ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                         SEQ ID NO 4
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: FASTEM: DOS
COFRATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
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US-09-608-810A-4
Sequence 4, Application US/09608810A
PARLED INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEFTIDES
FILE REFRENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
PAPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymcGenetics, Inc.
STREET: 1201 Eastlake Avenue East
1 ALAGWLRPEDGGQAEGAEDELEV 23
                         52 ALAGWLRPEDGGQAEGAEDELEV 74
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                                                                                                                                                        ; Sequence 2, Application US/08822897C
; Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SAWISIAK, DEDOTAH A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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STATE: WA
                                                                                                                                US-08-822-897C-2
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1998-05-07 1998-05-08 1998-05-28 1998-06-02 1998-06-02 1998-06-02 1998-06-02 1998-06-02 1998-06-02 1998-06-02 1998-06-03 1998-06-03 1998-06-03 1998-06-03 1998-06-04	NUMBER: 60 19988-06-00 19988-06-00 19988-06-00 19988-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00 1998-06-00	NUMBER: 60 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1 1098-06-1
APPLICATION APPLICATION APPLICATION FILING DATE: FILING DATE: FILING DATE:	PPLICATION ILING DATE	PELICATION ILING DATE ILING DATE PELICATION ILING DATE PELICATION ILING DATE ILING DATE ILING DATE
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PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08904
PRIOR PILING DATE: 1998-66-19
PRIOR FILING DATE: 1998-66-19
PRIOR FILING DATE: 1998-66-19
PRIOR PRILING DATE: 1998-66-19
PRIOR FILING DATE: 1998-66-19
PRIOR FILING DATE: 1998-66-19
PRIOR FILING DATE: 1998-66-19
PRIOR PRILING DATE: 1998-66-12
PRIOR APPLICATION NUMBER: 60/09025
PRIOR PRILING DATE: 1998-66-22
PRIOR APPLICATION NUMBER: 60/09025
PRIOR PRILING DATE: 1998-66-23
PRIOR PRILING DATE: 1998-66-23
PRIOR PRILING DATE: 1998-66-24
PRIOR PRILING DATE: 1998-66-26
PRIOR PRILICATION NUMBER: 60/09069

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Sequence 16, Application US/08339152A
Sequence 16, Application US/08339152A
Sequence 16, Application US/08339152A
Sequence 10, Application US/08339152A
Setting Train Information:
APPLICANT: Tanal, Rudolph E.
APPLICANT: Tanal, Rudolph E.
APPLICANT: Rowacs, Dora M.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TAM PC compatible
SOFTWARE: PAtentIn Release #1.0, Version #1.25
GUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 1;
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                 Score 50; DB 1;
Pred. No. 16;
; Mismatches
                                       REFERENCE/DOCKET NUMBER: 0609.4120000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4120000
TELECOMINICATION INFORMATION:
TELEPHONE: 202-371-2600
                            36,688
                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 17:
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76.9%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            : 653 amino acids
amino acid
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233 GGRAEGGEDEEEV 245
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-339-152A-16
                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-339-152A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 10; Conserv
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TYPE: am
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
ETLE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27758
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Sequence 17, Application US/08339152A
Sequence 17, Application US/08339152A
Patent No. 564376
GERERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: KOVACS, DOTA M.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Meshington
                                                                                                                                                                            Gaps
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                                                                                                                            ; Score 121; DB 4; Length 117;
; Pred. No. 6e-11;
0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATIG SYZFEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-252-991A-27758
Sequence 27758, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEV 23
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT CAGANISM: Pseudomonas aeruginosa US-09-252-991A-27758
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                                                                                                                              100.0%;
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                                                                                                                         Query Match 100.0°
Best Local Similarity 100.0°
Matches 23; Conservative
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203 GWLRPQDGSRA 213
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Best-Local Similarity
The B; Conserva
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COUNTRY: U
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Sequence 10, Application US/08039198B

Sequence 10, Application US/08039198B

Sequence 10, Application US/08039198B

SEGUENCANT: CROWE, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRECAMBINANT PCR STRATEGY

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 653;
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ed. No. 17;
Mismatches 2
                                                                                                                                                                                                                                                                                                                   PRILICE TON UNBER: US 08/007,999
FILING DATE: 21-JAN.1993
PRIOR APPLICATION NUBER: US 07/872,642
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 07/930,022
ATONEX/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
RESPERENCE/POCKET NUMBER: 29,021
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50;
Pred. No.
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APPLICATION NUMBER: US/08/039,198B
FILING DATE: 29-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/689,276A FILING DATE: 06-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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76.98;
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amino acid
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                FILING DATE: 06-AUG-1 PRIOR APPLICATION DATA:
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                                                                STATE: C
COUNTRY:
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                                                                                                                        APPLICANT: Wasco, Wilma
APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzl, Rudolph
APPLICANT: Tanzl, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08689276A
Patent No. 5891991
GENERAL INFORMATION:
APPLICANT: WASCO, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2; Length 653; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0609.3520002/JAG/GKT
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APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-ANG-1992
ATTORNEY/AGENT INFORMATION:
                                                              Sequence 3, Application US/08007999B Patent No. 5851787
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 06(
TELECOMMUNICATION:
TELEPHONE: (202)371-2571
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76.9%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 10; Conserv
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Gaps

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19723
LENGTH: 428
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                                                                                                                                                                                                       0; Mismatches
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; Sequence 19723, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723
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                                                                                              ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 52.4%;
Matches 11; Conservative
      NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29700
LENGTH: 283
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Best Local Similarity 55.0%
Marches 11; Conservative
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                                                                          TYPE: PRT
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEICA ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23604
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. RUBENFILON: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 2
Pred. No. 4.4;
1; Mismatches
                                                                                   REGISTRATION, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-86
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-039-198B-10
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01744
FILING DATE: 08-OCT-91
ATTONNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23604, Application US/09252991A Patent No. 6551795
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; Sequence 29700, Application US/09252991A
; Patent No. 6551795
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Best Local Similarity 61.5
Matches 8; Conservative
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Matches 9; Conserv
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RESULT 15

US-09-252-91A-25921

Sequence 25911, Application US/09252991A

Sequence 25911, Application US/09252991A

Sequence 25911, Application US/09252991A

Sequence 2591795

GENERAL INFORMATION:

APPLICANTON:

APPLICANTON:

TITLE OF INVENTION:

ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NOS: 33142

SEQ ID NOS: 33142

SEQ ID NOS: 33142
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38.0%; Score 46; DB 4; Length 517;
Best Local Similarity 47.6%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 8; Indels
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                           2 LAGWLRPEDGGQAEGAEDEL 21
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25921
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           US-09-989-721-268
US-09-992-598-268
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US-09-999-735-268
US-09-991-181-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 121; DB 9;
.larity 100.0%; Pred. No. 8.3e-10;
Conservative 0; Mismatches 0;
                                                                                  US-09-989-730-268
US-09-990-436-268
US-09-993-687-268
US-09-989-734-268
                                                                                                                                                                     US-09-997-666-268
US-09-990-52-268
US-09-990-711-268
US-09-990-711-268
US-09-998-156-268
US-09-998-156-268
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US-09-993-667-268
US-09-997-428-268
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                                                                                                                                                                                                                                                                                                                                               US-09-990-443-268
US-09-991-854-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5. Application US/09853253
| Patent No. US20020055156A1
| GENERAL INFORMATION:
| APPLICANT: JASPERS, STEPHEN
| APPLICANT: SHEPPARD, PAUL
| APPLICANT: BISSHEN, THERESA
| TILLE OF INVENTION UNDHER: 60/203,300
| PRIOR APPLICATION UNDHER: 60/203,300
| PRIOR APPLICATION NUMBER: 60/203,300
| WHERE OF SEQ ID NOS: 28
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: FASTESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
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 ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 23; Conser
US-09-853-253-5
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LENGTH: 23
  TYPE: PRT
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Matches
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Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
                                                                               September 11, 2003, 17:26:32; Search time 14.0214 Seconds (without alignments)
239.348 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.ppp:*
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(cgn2_6/ptodata/1/pubpaa/USO10A_PUBCOMB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO10A_PUBCOMB.ppp:*
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(cgn2_6/ptodata/1/pubpaa/USO0NB.ppp:*
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-989-732-268
US-09-991-073-268
US-09-991-442-268
US-09-991-163-268
US-09-993-604-268
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US-09-794-987-2
US-09-853-253-2
US-09-989-722-268
US-09-989-723-268
US-09-989-723-268
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                                                                                                                                                                                                                      541936 segs, 145912426 residues
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                                                                                                                                                          1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 121; DB 9; Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 23; Conservative 0; Mismatches 0;
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100.0%; Score 121; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0;
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Patent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: BIEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zs1933-11ke Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37, 438
REFERENCE/DOCKET NUMBER: 97-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALAGWLRPEDGGGAEGAEDELEV 23
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TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 117 amino acids
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STRANDEDNESS: single
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                                                     COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>.
INFORMATION FOR SEQ ID NO: 2
   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-853-253-2
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100.0%; Pred. No. 8.7e-10;
tive 0: Mismatches 0; Indels
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100.0%; Pred. No. 8.3e-10;
Live 0; Mismatches 0;
                APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 281933-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 7
SEQ ID 
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APPLICANT: JASPERS, STEPHEN
APPLICANT: SHEPREND, PAUL
TOTAL BISHOP, PAUL
TITLE OF INVENTION: 281933-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GO/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 3.0
SSCID NO 4
LENGTH: 24
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STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEV 23
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Matches 23; Conservative
SHEPPARD, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
US-09-853-253-6
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Best Local Similarity
Matches 23; Conserva
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APPLICANT:
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ORGANISM:
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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088030

R APPLICATION NUMBER: 60/088033

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088126

R APPLICATION NUMBER: 60/088167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08876
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-16
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                           R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R PLILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088655
R RILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/088810

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088824

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088826

R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/08994
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APPLICATION UNDBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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APPLICATION UNMBER: 60/090252
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
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     APPLICATION NUMBER:
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APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: Wood, William I.
APPLICANT: Mood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG3
CURRENT APPLICATION NUMBER: 60/06/250
PRIOR APPLICATION NUMBER: 60/06/250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06/310
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/08/310
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-06-02
PRIOR PRIOR FILING DATE: 1998-06-02
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US-09-989-722-268
Sequence 268, Application US/09989722
Facart No. US20020072067a1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
52 ALAGWLRPEDGGQAEGAEDELEV 74
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
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1998-06-19

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TITLE OF INVENTION: Accide Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE PREPRENCE: P3730PLG2
CURRENT FILING DATE: 2011-11-19
PRIOR PLICATION NUMBER: 05/09/9877
PRIOR PLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PLICATION NUMBER: 60/06311
PRIOR PLICATION NUMBER: 60/065311
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PRIOR PLICATION NUMBER: 60/06570
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PRIOR PLICATION NUMBER: 60/08910
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DR APPLICATION NUMBER: 60/088029
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088030
DR FILING DATE: 1998-06-04
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DR APPLICATION NUMBER: 60/088336
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
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Kljavin, Ivar J.
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                                             APPLICANT: Ashkenazi, Avi J.
                                                                              Baker, Kevin P.
Botstein, David
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Best Local Similarity 100.0%; Pred. No. 4.2
Matches 23; Conservative 0; Mismatches
DR FILING DATE: 1998-06-22

DR APPLICATION NUMBER: 60/090349

DR FILING DATE: 1998-06-23

DR FILING DATE: 1998-06-23

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090431

DR APLICATION NUMBER: 60/090445

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090445

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DR APPLICATION NUMBER: 60/090445

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DR APPLICATION NUMBER: 60/090535

DR PILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090535

DR PILING DATE: 1998-06-24
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R FILING DATE: 1998-06-25

RR APPLICATION NUMBER: 60/090662

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-07-01

R RILING DATE: 1998-07-01

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R APPLICATION NUMBER: 60/091549

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R APPLICATION NUMBER: 60/09159

R FILING DATE: 1998-07-01

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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090678
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
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R APPLICATION DATE: 1998-06-25
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R APPLICATION NUMBER: 60/091978
R RELING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R RILING DATE: 1998-07-07
R RAPLICATION NUMBER: 60/09182
R RELING DATE: 1998-07-07
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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; Sequence 268, Application US/09989723 ; Patent No. US20020072092A1

US-09-989-723-268

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PRIOR APPLICATION NUMBER: 60/088167
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PAPLICATION NUMBER: 60/088212
PRIOR PLING DATE: 1998-06-05
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PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088734
PRIOR PELING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08874
PRIOR PELING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/08940
PRIOR PELING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-16
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PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
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PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08960
PRIOR FILING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-23
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Gaps ö Length 117; Indels Query Match
100.0%; Score 121; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0; PRIOR FILING DATE: 1998-06-24
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PRIOR PELLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09059
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091478
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PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09193
PRIOR PELING DATE: 1998-07-07
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52 ALAGWLRPEDGGQAEGAEDELEV 74

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Sequence 268, Application US/09989279; Patent No. US20020072496A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Botstein, David; APPLICANT: Botstein, David; APPLICANT: Eaton, Dan L.; APPLICANT: Ferrara, Napoleone US-09-989-279-268 RESULT 8

1998-06-10

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A PPLICATION NUMBER: 60/08836
A PPLICATION NUMBER: 60/08836
A PILING DATE: 1998-06-10
A PILING DATE: 1998-06-11
A APPLICATION NUMBER: 60/08881
A RELING DATE: 1998-06-11
A APPLICATION NUMBER: 60/08881
A PILING DATE: 1998-06-11
A APPLICATION NUMBER: 60/088861
A PILING DATE: 1998-06-11
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R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089650
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089610
R FILING DATE: 1998-06-18
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R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
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R APPLICATION NUMBER: 60/089907
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R FAPLICATTON NUMBER: 60/090252
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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                                                                                                       APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/08824
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FILING DATE: 1998-06-23
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                           LING DATE: 1998-06-0
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC56
CURRENT FILING DATE: 2001-11-19
PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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R FILING DATE: 1998-06-03
R PILING DATE: 1998-06-04
R RILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
R RELING DATE: 1998-06-04
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R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087759
R FILING DATE: 1998-06-02
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088029
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R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-06-04
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R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/075945
R FILING DATE: 1998-02-25
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R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
F FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
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PILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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FILING DATE: 1998-03-20
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FILING DATE: 1998-06-04
                                                                                                  Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Good, William I.
                        Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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R APPLICATION NUMBER: 60/088212
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088738
                                                                                               Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                   Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
   Napier, Mary A.
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Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0;
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Patent No. US/0020072497A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botsein, David
APPLICANT: Eaton, David
                                                                                                   PRIOR FILING DATE: 1998-00-24
PRIOR FILING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/090547
PRIOR APPLICATION NUMBER: 60/09057
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
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PRIOR PILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-03
             R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

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DR APPLICATION NUMBER: 60/090542

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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PLICATION NUMBER: 60/090472
LING DATE: 1998-06-24
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US-09-989-727-268
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R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/088824
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R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
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R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090444
R RILING DATE: 1998-06-24
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R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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NG DATE: 1998-06-23
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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Sequence 268, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION: Godowski, Paul[†]J. Grimaldi, J.Christopher Gurney, Austin L. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Ferrara, Napoleone Fong, Sherman Gerritsen, Mary E. Goddard, Audrey Pan, James Paoni, Nicholas F. Gerber, Hanspeter APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L. Kljavin,Ivar J. Napier, Mary A. US-09-989-731-268 APPLICANT:
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
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PRIOR APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
                                 Williams, P. Mickey
Wood, William I.
Watanabe, Colin K.
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/989,732 CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/065311
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PRIOR PAPLICATION NUMBER: 60/06750
PRIOR PAPLICATION NUMBER: 60/075945
PRIOR PAPLICATION NUMBER: 60/08132
PRIOR PAPLICATION NUMBER: 60/08120
PRIOR PAPLICATION NUMBER: 60/08121
PRIOR PAPLICATION NUMBER: 60/08121
PRIOR APPLICATION NUMBER: 60/08121
PRIOR PAPLICATION NUMBER: 60/08121
PRIOR PLING DATE: 1998-06-04
PRIOR PAPLICATION NUMBER: 60/08121
PRIOR PLING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/088127
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APPLICATION UNMBER: 60/088861
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APPLICATION NUMBER: 60/088876
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4.2e-09;
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100.0%; Pred. No. 4.2
:1ve 0; Mismatches
                                                        R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25

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R APPLICATION NUMBER: 60/090695

R APPLICATION NUMBER: 60/090862

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RR FILING DATE: 1998-07-01

NR APPLICATION NUMBER: 60/091519

NR FILING DATE: 1998-07-02

NR APPLICATION NUMBER: 60/091626

R FILING DATE: 1998-07-02
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Patent No. US20020123463A1
GENERAL INFORMATION:
                      069060/09
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Ferrara, Napoleone
                                        FILING DATE: 1998-06-25
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Paoni, Nicholas F.
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23; Conservative
                    APPLICATION NUMBER:
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Matches 23
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PRIOR PELING DATE: 1998-06-16
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PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08908
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-20
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C15 Gaps ö Length 117; Indels ; DB 10; 4.2e-09; hes 0; 100.0%; Score 121; D 100.0%; Pred. No. 4.2 Live 0; Mismatches CURRENT APPLICATION NUMBER: US/09/991,073 CURRENT FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/049787 REFLIENCE DATE: 1998-06-25

RAPPLICATION NUMBER: 60/090862

RRAPLICATION NUMBER: 60/090863

RRAPLICATION NUMBER: 60/090863

RRAPLICATION NUMBER: 60/091360

RELING DATE: 1998-06-26

RELING DATE: 1998-07-01

RRAPLICATION NUMBER: 60/09154

RELING DATE: 1998-07-02

RRELING DATE: 1998-07-02 52 ALAGWLRPEDGGQAEGAEDELEV 74 1 ALAGWLRPEDGGQAEGAEDELEV 23 ; Sequence 268, Application US/09991073; Patent No. US20020127576A1 ; GENERAL INFORMATION: Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/065186 Napler, Mary A. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Watanabe, Colin K. Williams, P. Mickey Wood, William I. Ferrara, Napoleone Fong, Sherman Gerber, Hanspeter Kljavin, Ivar J. APPLICANT: Ashkenazi, Avi J. Conservative Botstein, David Baker, Kevin P. Desnoyers, Luc Tumas, Daniel 2hang, 2emin Eaton, Dan L Query Match Best Local Similarity Matches 23; Conserva US-09-991-073-268 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT PRIOR LANGE g

-11-12 -11-13 -11-13 -11-13 -11-24 -11-24 -10-25 -10-32		1998-06-05 NUMBER: 60/08865 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08874 1998-06-10 NUMBER: 60/08881 1998-06-10 NUMBER: 60/08885 1998-06-10 NUMBER: 60/08865 1998-06-11 NUMBER: 60/08865 1998-06-11 NUMBER: 60/08865 1998-06-11 NUMBER: 60/08867 1998-06-11 NUMBER: 60/08967 1998-06-11
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PRIOR APPLICATION NUMBER: 60/089514
PRIOR FLILING DATE: 1998-06-17
PRIOR PLILON DATE: 1998-06-18
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PRIOR PLILON DATE: 1998-06-24
PRIOR PLILON DATE: 1998-06-25

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R APPLICATION NUMBER: 60/083328
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R FILING DATE: 1998-04-28
R FILING DATE: 1998-05-28
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087607
R APPLICATION NUMBER: 60/087607
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/08727
R APPLICATION NUMBER: 60/08727
R APPLICATION NUMBER: 60/08021
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088028
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R APPLICATION NUMBER: 60/088655

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APPLICATION NUMBER: 60/089512
FILING DAPE: 1998-06-16
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APPLICANT: Abang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06510
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
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Best Local Similarity 100.0%; Score 121; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091637
PRIOR APPLICATION NUMBER: 60/091637
PRIOR PAPLICATION NUMBER: 60/091637
PRIOR PRILING DATE: 1998-07-07
PRIOR PRILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
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US-09-90-442-268
US-09-90-442-268
Sequence 268, Application US/09990442
Parent No. US2002013225241
GENERAL INFORMATION:
APPLICANT: ASHRENAZIANI J.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Napier, Mary A.
Pan, James
Paoni, Nicholas F.
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Botstein, David
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R APPLICATION NUMBER: 60/090557

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R FILING DATE: 1998-06-25

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R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/08952
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090431
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APPLICATION UNMBER: 60/090862
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                   Length 117;
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                                                                                                                                                                                                                 100.0%; Score 121; D
100.0%; Pred. No. 4.2
Live 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
            PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PELICATION NUMBER: 60/06770
PRIOR PILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                  1 ALAGWLRPEDGGQAEGAEDELEV 23
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Patent No. US20020113253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-04-28
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity 100.(
Matches 23; Conservative
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Napier, Mary A.
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Botstein, David
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US-09-991-163-268
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1998-05- NUMBER: 6 1998-06- 1998-06- NUMBER: 6 NUMBER: 6 1998-06- NUMBER: 6 1998-06- NUMBER: 6 1998-06- 1998-06- 1998-06- NUMBER: 6	1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08803 1998-06-04 1998-06-04 1998-06-04 NUMBER: 60/08816 1998-06-05 NUMBER: 60/08821 1998-06-05 NUMBER: 60/08821 1998-06-05 NUMBER: 60/08821 1998-06-05 NUMBER: 60/08821 1998-06-05 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08881	1998-06-11 1998-06-11 1998-06-11 1998-06-11 1998-06-12 NUMBER: 60/089105 1998-06-12 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089514 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959 1998-06-17 NUMBER: 60/08959
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PRIOR PLING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/08908

PRIOR PLING DATE: 1998-06-18

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PRIOR PLING DATE: 1998-06-19

PRIOR PLING DATE: 1998-06-22

PRIOR PLING DATE: 1998-06-23

PRIOR PLING DATE: 1998-06-24

PRIOR PLING DATE: 1998-06-26

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R APPLICATION NUMBER: 60/088742

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088810

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R APPLICATION NUMBER: 60/088826

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088858

R FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

DR APPLICATION NUMBER: 60/089876

DR FILING DATE: 1998-06-12

DR APPLICATION NUMBER: 60/08936

R FILING DATE: 1998-06-12

DR APPLICATION NUMBER: 60/089512

DR FILING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089512

DR FILING DATE: 1998-06-16

DR APPLICATION NUMBER: 60/089513

DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089599
                            PR FILING DATE: 1998-06-03

R APPLICATION NUMBER: 60/088021

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088028

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R FILING DATE: 1998-06-04

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R FILING DATE: 1998-06-05
RR APPLICATION NUMBER: 60/088217
RR FILING DATE: 1998-06-05
RR APPLICATION NUMBER: 60/088655
RR FILING DATE: 1998-06-09
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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      APPLICATION NUMBER: 60/087827
      PRIOR HELDER HEL
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APPLICANT: Roy, MAIGATER AND
APPLICANT: Tunedry A.
APPLICANT: Tunedry A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Colin K.
APPLICANT: Applicant Colin K.
APPLICANT: Applicant Colin K.
APPLICANT: Accorded and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                            Length 117;
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Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/049787

PRIOR PLING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/06250

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/06570

PRIOR PELING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/078910

PRIOR PELING DATE: 1999-10-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR APPLICATION NUMBER: 60/078910

PRIOR APPLICATION NUMBER: 60/08312

PRIOR APPLICATION NUMBER: 60/08320

PRIOR APPLICATION NUMBER: 60/08320

PRIOR PELING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/08160

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PRIOR APPLICATION NUMBER: 60/08160

PRIOR PELING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087609

PRIOR PELING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087699

PRIOR APPLICATION NUMBER: 60/087699

PRIOR APPLICATION NUMBER: 60/087599

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PRIOR PELING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J. Christopher
Gurney, Austin L.
Kljatin, Ivar J.
Napier, Mary A.
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Pan, James
Paoni, Nicholas F.
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Goddard, Audrey
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Botstein, David
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/090246
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR PLING DATE: 1998-06-24
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PRIOR PRIOR DATE: 1998-07-02
PRIOR PRIOR PRIOR DATE: 1998-07-02
PRIOR PRIOR PRIOR DATE: 19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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Gaps

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Length 117; Indels

Ouery Match 100.0%; Score 121; DB 10; Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 23; Conservative 0; Mismatches 0;

1 ALAGWLRPEDGGQAEGAEDELEV 23 셤 õ

Search completed: September 11, 2003, 17:48:32 Job time : 15.0214 secs



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 11, 2003, 17:21:03 ; Search time 8.60963 Seconds (without alignments) 256.908 Million cell updates/sec

US-09-853-253-5 121 Title: Perfect score:

1 ALAGWLRPEDGGQAEGAEDELEV 23 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	qhrelin precursor	qhrelin precursor	nucleoplasmin - Af	probable transcrip	hypothetical prote	conserved hypothet	chloride channel p	chloride channel;	hypothetical prote	amyloid precursor-	amino acid ABC tra	exfoliative toxin	hypothetical prote	Na+/Ca2+,K+-exchan	protein kinase PK1	kappa opioid recep	unknown protein F2	hypothetical prote			protein containing	xylan beta-1,4-xyl	hypothetical prote	matrix metalloprot	matrix metalloprot	matrix metalloprot	cold-shock domain	ribosomal protein	Os ribosomal prot
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SUMMARIES	ΩI	A59316	B59316	A26169	683609	T21920	B69811	AE2760	C97541	B75433	A46362	C75609	A26050	T49338	820969	T09738	A55259	C96767	T26398	A87377	C82965	н97088	C84110	B71039	I38028	I48673	I84471	C87574	T43321	S62409
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	Query Match Length DB	117	117	200	232	249	91	604	604	131	653	484	274	114	1199	355	380	1273	80	259	287	491	528	871	582	582	583	69	184	191
dР	Query	100.0	74.4	44.6	43.0	42.6	42.1	42.1	42.1	41.3	41.3	40.9	40.5	39.7	39.7	38.8	38.8	38.8	38.4	38.0	38.0	38.0	38.0	38.0	37.6	37.6	37.6	37.2	37.2	37.2
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δ g RESULT 2 B59316

by State names: preproghrelin
Ny Alternate names: preproghrelin
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Accession: B59316
R; Kojima, M; Hosoda, H; Date, Y; Nakazato, M; Matsuo, H; Kangawa, K.
Nature 402, 656-660, 1999
A; Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A; Reference number: A59316, MUID: 20067959; PMID: 10604470
A; Accession: B59316
A; Status: not compared with conceptual translation
A; Molecule type: mRNA; protein
A; Molecule type: mRNA; protein
A; Mosidues: 1-17 - KOJ)
A; Cross references: GB: AB029433; NID: 96691569; PIDN: BAA89370.1; PID: 96691570
A; Experimental source: strain SD; tissue stomach endocrine cells

CCAAT-binding fact hypothetical prote hypothetical prote potassium channel. CTP synthase - Dei ATP-binding protei inner membrane ABC sucrose-phosphate ral guanine nucleo major core protein probable tryptopha vertebrate NK-2 ho hypothetical prote algs protein (ABC) chromogranin A pre mocR protein - Dei	#te Mats 11s 11s 11s 11s tes tus	121; DB 1; Length 117; No. 4.2e-10; natches 0; Indels 0; Gaps 0;
S67270 G71446 G71446 UC519446 UC51919 B75379 T17436 T17436 T174994 T44994 UC4634 AC2960 C98323 AA1520 A75353	RESULT 1 Spide and precursor - human NyAlternate names: preproghrelin C:Species: Homo saplens (man) C:Species: Homo saplens (man) C:Accession: A59316 R:KOjima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Mature 402, 656-660, 1999 A:Title: Ghrelin is a growth-hormone-releasing acy A; Reference number: A59316; MUID:20067959; PMID:10 A; Reference number: A59316; MUID:20067959; PMID:10 A; Reference number: A59316; MUID:20067959; PMID:10 A; Residues: 1-117 KNOJ- A; Residues: 1-117 CKOJ- A; Residues: 1-117 Chanal translation A; Mote: submitted to GenBank, June 1999 C; Superfamily: motilin C; Superfamily: mot	Score Pred. 0; Misr
0000000000000000	hrelin nce_revisi Date, Y.; th-hormone ; MUD:200 h conceptu h conceptu nk, June 1 dby the s trotein; steence #stain status pre terminal F te (Ser) (100.0%; 100.0%; ive
242 296 297 297 297 200 1059 1059 1033 1033 1034 1049 449	human lens (man) lens (man) #sequence_revis a, H; Date, Y; 1999 a growth-hormor A59316; MUID:20 red with concept NA Sequence tissue stome ce: tissu	vat
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44 4444444 4444444 4444444444444444444	SULT 1 Alternate names: preproghrelin Species: Homo saplens (man) Date: 16-Jun-2000 #sequence_rev Kodjim, M.; Hosdoa, H.; Date, Y ture 402, 656-660, 1999 Title: Ghrelin is a growth-horm Reference number: A59316; MUID: Residues: not compared with concep Molecule type: mRNA Residues: 1-117 < KOJ> Cross-references: GB:AB029434; b Experimental source: tissue ston Note: submitted to GenBank, June Comment: Ghrelin secreted by th Superfamily: motilin Superfamily: motilin Superfamily: motilin Superfamily: signal sequence#si 24-51/Product: ghrelin #status i 25-117/Domain: carboxyl-termina,	Match Local Sin les 23;
0 11 12 18 18 18 18 18 18 18 18 18 18 18 18 18	RESULT 1 A59116 A59116 A59116 C) Species: homo sapiens (man) C) Species: homo sapiens (man) C) Date: 16-Jun-2000 #sequence_revis C) Accession: A59316 R;Kojima, M; Hosoda, H; Date, Y; Nature 402, 656-660, 1999 A;Title: Ghrelin is a growth-hormor A;Reference number: A59316; MUID:2(A;Accession: A59316; MUID:2(A;	Query Match Best Local Matches 2

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A;Cross-references: EMBL:275540; PIDN:CAA99852.1; GSPDB:GN00019; CESP:F37D6.7 A;Experimental source: clone F37D6 C;Genetics:
                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21920
R;McMurray, A.
                                                                                                                                                                             hypothetical protein F37D6.7 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, June 1996
A; Reference number: 219487
A; Accession: T21920
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-249 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:F37D6.7
A;Map position: 1
A;Introns: 41/1; 62/1; 115/1; 176/1; 209/1
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73 WIRPETNGGDDDGSEDK 89
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52.9%;
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Best Local Similarity 52.99
Matches 9; Conservative
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C;Superfamily: acylphosphatase
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A; Note: submitted to GenBank, June 1999
C; Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt C; Superfamily: motilin
C; Keywords: hormone; lipoprotein; stomach
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-51/Product: ghrelin status predicted <MATP>
F; 24-51/Product: ghrelin status propeptide #status predicted <CTP>
F; 26/Binding site: octanoate (Ser) (covalent) #status experimental
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C;Species: Xenopus lacvis (African clawed frog)

C;Species: Nenopus lacvis (African clawed frog)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999

C;Accession: A26169

E;Dingwall, C: Dilworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.

END J. 6, 69-74, 1987

A;Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of shacession: A26169

A;Reference number: A26169

A;Accession: A26169

A;Residues: 1-200 <DIN>
A;Residues: 1-200 <DIN>
A;Residues: 1-200 <DIN>
A;Residues: 1-200 <DIN>
C;Superfamily: nucleophosmin

C;Superfamily: nucleophosmin

C;Keywords: molecular chaperone; nucleus
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Pred. No. 5.4;
2; Mismatches 1; Indels
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Local Similarity 55.6%; Pred. No. 2.4;
108 10; Conservative 2; Mismatches 6; Indels
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C; Genetics:
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Best Local Similarity
Matches 8; Conserva
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A;Experimental source: strain 168
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                Gaps
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          5.
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          5; DB
6.9;
Score 51.5; DB
Pred. No. 6.9;
5; Mismatches
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A; Molecule type: DNA A; Residues: 1-131 <WHI>
A; Residues: 1-131 <WHI>
C; Cross-references: GB: AE001963; GB: AE000513; NID: g6458869; PIDN: AAF10714.1; PID: g645
A; Experimental source: strain R1
C; Genetics:
C; Genetics: A; Map position: 1
C; Superfamily: Deinococcus radiodurans hypothetical protein DR1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Mus musculus (house mouse)
C;Date: 21.5ep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A46362
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-1078, 1992
A;Tille: Identification of a mouse brain DNA that encodes a protein related to the A A;Reference number: A46362; MUID:93066322; PMID:1279693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: sequence inconsistent with the nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684) C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C; Keywords: transmembrane protein
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A;Experimental source: strain Rl
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Pred. No. 29;
1; Mismatches 2; Indels
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Pred. No. 26;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                          Score 50; DB;
Pred. No. 5.9;
2; Mismatches
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76.9%;
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Best Local Similarity 61.1%;
Matches 11; Conservative
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233 GGRAEGGEDEEEV 245
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A;Molecule type: nucleic acid
A;Residues: 1-653 <WAS>
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Matches 10; Conservative
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A; Residues: 1-484 <WHI>
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A; Status: preliminary
      A;Status: preliminary
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A;Gene: DRA0136
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C75609
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C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Accession: C97541
R; Goddner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 232-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
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C.; Ma
                                                                               C; Accession: AE2760
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I stage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell: Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
chloride channel protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R. Witch, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R. Sinth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Delnococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                              ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Recession: AE2760
A/Status: preliminary
A/Roccus preliminary
A/Roccus in C64 KUR>
A/Residues: 1-604 KUR>
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
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ed. No. 20;
Mismatches
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illarity 62.5%; Pred. No. 20;
Conservative 1; Mismatches
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A;Gene: clc
A;Gene: clc
A;Map position: circular chromosome
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A;Map position: circular chromosome
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Best Local Similarity
Matches 10; Conserva
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A;Molecule type: DNA
A;Residues: 1-604 <KUR>
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us-09-853-253-5.rpr

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1199 <REI>
A;Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579
                                                                                                           Query Match
Best Local Similarity 45.v.
9; Conservative
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Na+/Ca2+,K+-exchanger
Na/Ca2+,K-exchanger
C;Shecies: NayCa,K-exchanger
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Caccession: S20969
R;Rellaender, H ; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
EMBO J. 11, 1689-1695, 1992
EMBO J. 11, 1689-1695, 1992
A;Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovin A;Reference number: $20969; MUID:92258377; PMID:1582405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
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                                                                                                                                                                                                                                              C;Species: Staphylococcus aureus
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 18-Nov-2002
C;Accession: A26050
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C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C.Accession: T49338
                                                                                                                                                                                                                                                                                                                        R.Jackson, M.P.; Iandolo, J.J.
J. Bacteriol. 167, 726-728, 1986
A;Title: Sequence of the exfoliative toxin B gene of Staphylococcus aureus.
A;Reference number: A26050; MUID:86277939; PMID:3733674
A;Accession: A26050
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-114 <SCH>
A; Cross-references: BMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.230
A; Experimental source: BAC clone B13N20; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: Neurospora crassa hypothetical protein B13N20.230
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44.4%; Pred. No. 17;
tive 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: 1-274 < 47AC> C; Superfamily: staphylococcal serine proteinase F; 1-31/Domain: staphylococcal serine predicted <SIG> F; 1-31/Domain: stapinal sequence #status predicted <MAT> F; 32-274/Product: exfoliative toxin B #status predicted <MAT>
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9.9;
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Pred. No.
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86 WLKIQDGGDTTGQEEQPE 103
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468 LAGWLTPR-GLRAEGGEE 484
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                            2 LAGWLRPEDGGQAEGAED 19
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 10; Conservative
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Matches 8; Conserv
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A;Gene: NCSP:B13N20.230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 6
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S20969
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C;Accession: T09738
R;Heino, P.; Nylander, M.; Palva, T.; Bartels, D.
submitted to the EMBL Data Library, April 1998
A;Description: Isolation of a CDNA corresponding to a protein kinase differentially e
A;Reference number: 216839
A;Accession: T09738
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                                                                                                                                                                                                                                                 profein kinase PK1 (EC 2.7.1.-) - Craterostigma plantagineum
C;Species: Craterostigma plantagineum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase homology
                                                 Gaps
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    Length 1199;
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                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: kinase-related transforming protein; C;Keywords: ATP; phosphotransferase; protein kinase F;2-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-355 <HEL>
A,Cross-references: EMBL:AJ005373
C,Genetics:
Score 48; DB 2;
Pred. No. 1e+02;
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Pred. No. 43;
4; Mismatches
                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 11, 2003, 17:26:24 Job time : 9.60963 secs
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                                                                                                                      | :: :||: || ||| |:
816 GEIQAGEGGEVEGDEDEGEI 835
                                                                                            4 GWLRPEDGGQAEGAEDELEV 23
  39.7%;
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Best Local Similarity 37.0%;
Matches 10; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein . protein search, using sw model

September 11, 2003, 17:21:03 ; Search time 3.32086 Seconds
(without alignments)
325.703 Million cell updates/sec Run on:

US-09-853-253-5 121 1 ALAGWLRPEDGGQAEGAEDELEV 23 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description	Ogubu 3 homo sanion			Snm		Q9bef8 canis famil		035031 bacillus su	~		Q8tx28 methanopyru	Q28139 bos taurus	P41144 cavia porce		Q9xt90 sus scrofa	P50281 homo sapien	P53690 mus musculu		P49023 homo sapien	Q09757 schizosacch	Q02516 saccharomyc		-	Q92543 homo sapien	Q43876 vicia faba	O15211 homo sapien	P15024 recvirus (t	Q9w7r2 verasper mo	Q944w6 brassica ol	P42586 mus musculu	P05059 bos taurus		O9rxel deinococcus
SUMMARIES	ID	GHRL HIMAN	GHRL RAT	GHRL PIG	GHRL_MOUSE	GHRL_BOVIN	GHRL_CANFA	NUPL_XENLA	ACYP_BACSU	APP1_MOUSE	NKX1_BISBI	SYM_METKA	NKX1_BOVIN	OPRK_CAVPO	DDX8_ARATH	MM14_PIG	MM14_HUMAN	MM14_MOUSE	MM14_RAT	PAXI_HUMAN	RS9A_SCHPO	HAP5_YEAST	KCF1_HUMAN	PYRG_DEIRA	SNXJ_HUMAN	SPS_VICFA	RGL2_HUMAN	VL1_REOVD	INS_VERMO	TCTP_BRAOL	NK22_MOUSE	CMGA_BOVIN	PKSK_BACSU	SYK_DEIRA
	Duery Match Length DB	117 1	_		117 1		117 1	200 1	91 1	653 1	300	668 1	1216 1	380 1	1168 1	580 1	582 1	582 1	582 1	591 1	190 1	•		•	•	• •	777 1	•	•	168 1	273 1	449 1	4447 1	525 1
ď	Query Match	100.0	74.4	71.9	71.1	9	26.2	44.6	42.1	41.3	39.7	39.7	39.7	38.8	38.8	37.6	37.6	37.6	37.6	37.6	37.2	37.2	37.2	37.2	37.2	37.2	9	vo.	യ	36.4	36.4			36.0
	Score	121	90	87	98	72	68	54	51	20	48	48	48	47	47	45.5	45.5	45.5	45.5	•	4.5	4.5	45	4	45	4	4	44.5	44		44	44	44	43.5
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Q95220 oryctolagus Q9d5v6 mus musculu	P41145 homo sapien Q8pnz5 xanthomonas	P16230 oryctolagus P96142 thermus the	P29376 homo sapien P54423 bacillus su	P38631 saccharomyc P01341 lophius p1s	P05019 homo sapien	P27484 nicotiana s
MM14_RABIT SYAP_MOUSE	OPRK_HUMAN SYQ_XANAC	SRCH_RABIT SYV_THETH	KLTK_HUMAN WPRA_BACSU	GLS1_YEAST	IGFB_HUMAN	GRP2_NICSY
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582 365	380 579	852 862	864 894	1876	195	214
36.0	35.5 35.5	35.5 35.5	35.5	35.5	35.1	35.1
43.5	43 43	4 4 8 3	4 4 3	43	42.5	42.5
34 35	36 37	3 8 3 8	40	4 4 3 8	44	45

ALIGNMENTS

ALLGNAENTO	GHRL_HUMAN STANDARD; PRT; 117 AA.	28-FEB-2003 (Rel		Homo sapiens (Human). Eukaryota; Metazoa; Chordata;		SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-Z6. MEDLINE=20067959; Pubmed=10604470;	RA KOjima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.; RT "Ghrelin is a growth-hormone-releasing acvlated peptide from		KL NG LUTE 402:030-000(1339). RN [2]		KA KOJIMA M.; RI. Suhmitted (DEC-1999) to the EMRL/CenBank/DDB.I databases	[3]	RP SEQUENCE FROM N.A. (ISOFORM 1).	RT "Identification of a novel gastric protein m46.";	RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.		RT "Genomic organization of the human Ghrelin gene."; Dr. I Budocrinol Canat 1:231-233/2000.		RC TISSUE=BIOOG; BY MEDIINE=22388257: DubMed=12477032:		ka Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hobkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S. Loguellano N.A. Peters G.T. Abramson R.D., Mullahy S.T.		RA VILIAION D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs K.A., Da Fahaw T Wolton F Kottoman M Madan A Bodriffings S Sanchom A		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
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Gaps

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Length 117; Indels

Score 121; DB 1; Pred. No. 1.5e-10;

100.0%; 100.0%;

Mismatches

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Conservative

23;

117 AA; 12911 MW; 39C0572EBECA2755 CRC64;

SEQUENCE

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Query Match
Best Local Similarity
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Name=1; Synonyms-chrelin;
Isolad-090403-1; Sequence=bisplayed;
Name=2; Synonyms-del-Gln14-ghrelin;
Isola-090403-2; Sequence=VSP_003245;
FTM: Or-octanolation is essential for activity.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infoblogen.fr/services/chromcancer/Genes/GhreliniD327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; 00:0005615; C:extracellular space; TAS.
GO; 00:0005625; C:soluble fraction; TAS.
GO; GO:00056131; F:growth hormone receptor ligand activity; TAS.
GO; GO:0007267; P:cell-signaling; TAS.
GO; GO:0007186; P:C-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR006737; motilin_gassoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                                                                                                                                                                      ichnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Probom; PR01624; GHRELIN.
Probom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                           Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2).
/FTId-VSP_003245.
L -> M (IN REF. 5).
                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                            TISSUE-Stomach; MEDLINE-20389976; Pubmed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB029434; BAA89371.1; --
EMBL, AJ252278; CAB65733.1; --
EMBL, AF296558; AAG10300.1; --
EMBL, AF296558; AAG10300.1; --
EMBL, BC022791; AAH25791.1; --
PIR; A59316; A59316.
                                                                                                                                                                                                                                                                                                                                                                                    growth requlation.
                                                                             SEQUENCE OF 24-33.
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hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
Trends Endocrinol. Metab. 12:118-122(2001).
Trends Endocrinol. Metab. 12:118-120 (2001).
Trends Endocrinol. Metab. 12:118-120 (2001).
Treceptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoda H., Kojima M., Matsuo H., Kangawa K.; "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide in gastrointestinal tissue."; In gastrointestinal tissue."; Blochem. Biophys. Res. Commun. 279:909-913(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER.26.
STRAIN-Sprague-Dawley; TISSUE-Stomach;
MEDLINE-20067959; PubMed-10604470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-11433488; PubMed-11549267;
Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Srructure-activity relationship of ghrelin: pharmacological study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.,
Gibrelin is a growth-hormone releasing acylated peptide from
stomach ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endogenous ligand for the growth hormone secretagogue receptor.";
J. Biol. Chem. 275:21995-22000(2000),
                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hosoda H., Kojima M., Matsuo H., Kangawa K.; "Purification and characterization of rat des-Gln14-ghrelin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 287:142-146(2001)
                                                                                                                                        117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Stomach; MEDLINE-20357315; PubMed-10801861;
1 ALAGWLRPEDGGQAEGAEDELEV 23
                    52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth regulation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                           Q9QYH7; Q9ET69;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402:656-660(1999).
                                                                                                                                          STANDARD;
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MEDLINE-21092536;
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                                                                                                                                          GHRL_RAT
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                                                                                               RESULT 2
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
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72
118 AA;
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53
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38
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
Name-1; Synonyms-Ghrelin; Isola-GoyUH7-1; Sequence-Displayed; Isola-GoyUH7-2; Sequence-Displayed; Isola-O9OYH7-2; Sequence-VSP_003248; Isola-O9OYH7-2; Isola-O9O
                                                                                                                                                                                                                                                                                                           -I- MASS SPECTROMETRY: MW-3187.1; MW_ERR-0.6; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PD312162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHRL_PIG STANDARD; PRT; 118 AA.
09GKY5; Q9BDG8; Q9GKY4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2).
/FTId=VSP_003248.
8857546FE51A7691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 1; L
.4.1e-06;
                                                                                                                                                                                                                                                                                                                                     RANGE=24-36, 38-51.
-!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-OCTANOATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.4%; Score 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB035699; BAB11956 1; -.
PIR; B59316; B59316.
INTERPRO; IPRO06733; motilin_assoc.
InterPro; IPRO06738; motilin_ghrelin.
InterPro; IPRO05441; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB029433; BAA89370.1; -. EMBL; AB035699; BAB11956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t Local Similarity 73.9%;
ches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHRELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01624;
                                                                                                                                                                                                                                                                                 RANGE-24-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHRL_PIG
           g
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Rousselle J., Lacroix D., Dubreuil P.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                   Name-1; Synonyma-Ghrelin;
Isold-09GKY5-1; Sequence-Displayed;
Name-2; Synonyma-del-Gln14-ghrelin;
Isold-09GKY5-2; Sequence-VSP_003447;
-!- PTM: O-n-octanoylation is essential for activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMOVED IN MATURE FORM (BY SIMILARITY).
N-OCTANOATE (BY SIMILARITY).
Missing (in 1soform 2).
FTIA-082_003247.
L -> P (IN REF. 2; AAK30002).
K -> E (IN REF. 2; AAK30002).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHRL_MOUSE STANDARD; PRT; 117 AA.
09EQX0; 09WUZ1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Db 1,
J. 1.1e-05;
J. 1.1e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856D3E1D6DAB1A76 CRC64;
                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR006737; motilin_assoc.
Interpro; IPR006738; motilin_ghrelin.
Interpro; IPR005441; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF04643; motilin_assoc; 1.
Bran; PF04644; motilin_ghrelin; 1.
PRIMES; PR01664; GHRELIN
PRODOM; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB035704; BAB19049.1; -. EMBL; AF308930; AAK19243.1; -. EMBL; AY028942; AAK30002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB035703; BAB19048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.98;
65.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone; Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing
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A Kojima M., Hosoda H., Matsuo H., Kangawa K.;

MEDLINE-21203998; PubMed=11306316;

Thormone secretagogue receptor.";

Trends Endocrinol. Metab. 12:118-122(2001).

TRENDATIVE INCOMINON: Secreted.

TRENDATIVE PRODUCTS:

Event-Alternative Splicing; Named isoforms=2;

Name=1; Synonyms-detalin;

TSOId=09E0X0-1; Sequence-Displayed;

Name=1; Synonyms-del-Ginlid ghrelin;

TSOIG=09E0X0-2; Sequence-VSP 003246;

TSOIG=09E0X0-2; Sequence-VSP 003246;

TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract

With higher levels in the stomach, medium levels in the duodenum,

1 sylonym and colon. Low expression in the testis and brain.

THOM On-octanoylation is assential for activity (By similarity).

THARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara M., Nishia K., Kiyosawa H., Kondo S., Yamanaka I.,
A alto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Usons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbech C., Seya T., Shibata Y., Sotoch K.-F.,
A Suzuki H., Toyo-oka K., Wang K., Wang K., Wawaji H., Kohtsuki S.,
A Hayashizaki Y.;
Rhyshwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                              Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                 "Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Stomach;
MEDLINE-21085660; PubMed-11217851;
                       MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                            [2]
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                            Kojima M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVIEW
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                       PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (BY S N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                           5e-05; 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                              EACB49DZE3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                  FTIG-VSP_003246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
EMBL; AJ243503; CAB46500.1; -.
EMBL; AB0035701; BAB19046.1; -.
EMBL; AR006078; BAB55814.1; -.
EMBL; AK008668; BAB25814.1; -.
EMBL; AK008660; BAB25934.1; -.
MGD; MGT:1930008; Ghrl.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005776; C:extracellular; IDA.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR006738; motilin_assoc;
InterPro; IPR006738; motilin_ghrelin.
Pfam; PP04644; motilin_assoc; 1.
                                                                                                                                                                                                                                                                                                                                                                                             71.1%; Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                     GHRELIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHRL BOVIN STANDARD;
Q9BDJ6; Q9GKY6;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                               117 AA; 13207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 24-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 69.6
Matches 16; Conservative
                                                                                                                                                                                                                                                 Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Kita K., Harada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                   24
52
26
37
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                   PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHRL_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
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CAC29156.1;

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EMBL; AJ298296;
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                      VARSPLIC
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                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                     LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUPL_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11D
DD41D
D4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1; Synonyms=Ghrelin;
IsoId=09BEFB-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=09BEFB-2: Sequence=VSP_003244;
-!- PTM: O-n-octanoylation is essential for activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                               DASIC LESACT.
GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
N-OCTANOATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Gastric fundus;
Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
"Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                             residues; Signal; Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHRL_CANFA STANDARD; PRT; 117 AA.

Q9BEF8; Q9BEF7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1; Length 116;
Pred. No. 0.0015;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                          InterPro; IPR00673; motilin_assoc.
InterPro; IPR00673; motilin_assoc.
InterPro; IPR00673; motilin_ahrelin.
Pfam; PF04644; motilin_absoc; l.
Pfam; PF04644; motilin_absoc; l.
PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; l.
ProDom; PD332162; Preproghrelin; l.
ProDom; PD332162; Preproghrelin; l.
Propom; PD32162; Preproghrelin; l.
Propom; PD32162; Preproghrelin; l.
LIRID 23 GHRELIN (B)
PROPEP 51 116 REMOVED IN
LIPID 26 26 10 N-OCTRNOAIN
LIPID 26 26 IN
  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF350329; AAK18612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ298295; CAC29155.1; -
                                                                                                                                                                                                                                                                                                                                                  116 AA; 12792 MW;
                                                                                                                                                                                                                                                                                                                                                                                      59.5%;
                                                               BAB19047.1
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.2
es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9615;
                                                                 AB035702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHRL OR MTLRP
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fundus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
GHRL_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCC
CCC
DDR
DDR
DDR
FFT
FFT
SQ
SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         its developmental expression.";
Genes Dev. 1:97-107(1987).
-I- FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
AND TRANSFERRING THEM TO DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buerglin T.R., Mattaj I.W., Newmeyer D.D., Zeller R., de Robertis E.M.; "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and cluster of sequences homologous to putative nuclear localization signals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                       PRINTS; PRO1624; GHRELIN.
ProDom; P1313162: Preproghrelin; 1.
Hormone: Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dingwall C., Dilworth S.M., Black S.J., Kearsey S.E., Cox L.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117,
                                                                                                                                                                                                                                                                                                                           N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score bo; Pred: No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                      3E57FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: Homopentamer.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                             /FTId-VSP
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 7-200 FROM N.A. MEDLINE-88112783; PubMed #3428591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-87218476; Pubmed-2884102;
                                                                                                                                                                                                                                                ΒY
                                                                                                                                                                                                                                                                                                                                                                                                         13007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X04766; CAA28460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                              23
51
117
26
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 6:69-74(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleoplasmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laskey R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUPL_XENLA
P05221;
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Solomon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A KUNSET F., Ogasawara N., Mosser I., Albertini A.M., Alloni G., A KUNSET F., Ogasawara N., Mosser I., Abortini A., Borchert S., A Borriss R. Boursier L., Brans A., Fran M., Brignell S.C., Bron S., Broullet S., Bruschi C.V., Cadwell B., Capuano V., Carter N.M., A Broullet S., Eruschi C.V., Cadwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., A Britz C., Fujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Febret C., Ferrari B., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallaron N., A Gulseppi G., Guy B.J., Haga K., Glighliy E.J., Grandi G., Guspppi G., Guy B.J., Haga K., Halbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., A Kobayashi Y., Koetter P., Konlngstein G., Krogh S., Kunano M., Kurita K., Lapldus A., Lardinols S., Lauber J., Lazarevic V., Lazarevic V., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein."; Gene 194:191-199(1997).
                                                                                           HISTONE BINDING SITE).
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                 DB 1; Length 200;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                        A91DD110F2965812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
                                                                                                             D -> N (IN REF. 2)

E -> A (IN REF. 2)

N -> H (IN REF. 2)

A -> K (IN REF. 2)

A -> K (IN REF. 2)

T -> S (IN REF. 2)

L -> V (IN REF. 2)

L -> V (IN REF. 2)

MISSING (IN REF. 2)

C -> P (IN REF. 2)

C -> P (IN REF. 2)
                                                                                          CU (PROBABLE (IN REF. 2)
                                                                                Nuclear protein; Phosphorylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                        91 AA
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                Score 54; D
Pred. No. 1;
                      PDB; IEE5; 26-SEP-01.
PDB; IEC7; 24-APR-00.
PDB; IK5J; 21-NOV-01.
InterPro; IPRO04301; Nucleoplasmin.
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97417488; Pubmed-9272861;
                                                                                                                                                                                                                                                                                                       | || |:||| |:|
126 WAEEEDEGEAEGEEEEE 143
                                                                                                                                                                                                                                                                                           5 WLRPEDGGQAEGAEDELE 22
                                                                   Pfam; PF03066; Nucleoplasmin;
                                                                                                                                                                                                                           22023 MW;
                                                                                                                                                                                                                                               44.6%;
EMBL; Y00204; CAA68363.1;
PIR; A26169; A26169.
                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                      11
27
31
61
72
72
80
                                                                                                                                                                                                                147
200 AA;
                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-AC327
                                                                                                                                                                                                                                                                                                                                                                      ACYP_BACSU
035031;
                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
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CONFLICT
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                                                                                                    CONFLICT
                                                                                                                CONFLICT
                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                            ACYP_BACSU
                                                                                                                                                                                                                                                                     Matches
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Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
Riegar M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Raigar M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Rator T., Scanlan E., Schlach S., Schroeter R., Scoffone F.,
Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Sorokin A., Tamakoshi A., Tanaka T., Takahashi H., Takamaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vanniare F., Vassarotti A.,
Viari A., Wambutt R., Wadler E., Wedler H., Weltzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: An acyl phosphate + H(2)0 - a fatty acid anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APP1_MOUSE STANDARD; PRT; 653 AA.
003157; 08V038;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Amyloid-like protein 1 precursor (APLP) (APLP-1) (Contains: C30].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
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Solomon F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Complete proteome. SEQUENCE 91 AA; 10318 MW; 50795631BF3310F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001884; Acylphosphatase; 1. PROSITE; PS00150; ACYLPHOSPHATASE_1; 1. PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D86417; BAA22305.1; -.
EMBL; 299108; CAB12593.1; -.
PIR; B69811; B69811.
HSSP; PO0918; 1AP5; SubtiList; BG12947; yflt.
InterPro; IPR001792; Acylphosphatase.
Pfam; PF00708; Acylphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LAGWLRPEDGGO----AEGAEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00112; ACYLPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
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qq
                                                                                Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhet N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hatch F.,
An Hopkins R.F., Jordan H., Moore T., Mang J., Hsich F.,
An Hopkins R.F., Jordan H.S., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
An Eromastein M.J., Usdin T.B., Tonshyuki S., Carninci P., Prange C.,
An Brownstein M.J., Usdin T.B., Tonshyuki S., Carninci P., Prange C.,
An Richards S., McCham P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
An Hidhon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Huting M., Madan A., Young A.C., Scheckenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
An Huterfield Y.S.N., Krzywinski M.I., Sahaka U., Smailus D.E.,
An Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Thuman and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96139497; PubMed-8576160; Beher D., Hesse L., Masters C.L., Multhaup G.; Regulation of amyloid protein precursor (APP) binding to collagen and mapping of the binding sites on APP and collagen type I."; J. Biol. Chem. 271:1613-1620(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 277:44195-44201(2002).
-1- FUNCTION: May play a role in postsynaptic function. The C-terminal gamma-secretase processed fragment, ALIDI, activates transcription activation through APBAI (Re65) binding. Couples to JIP signal transduction through C-terminal binding. May interact with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99389880; PubMed-10460257; Homayouni R., Rice D.S., Sheldon M., Curran T.; "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22313598; PubMed-12228233;
Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
"Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
secretase regulates transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular G-protein signaling pathways. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I. FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of neuronal apoptosis (By similarity). SuBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB and APBA family members, MAPKBIP1 and Dabl (By similarity). Binding to Dabl inhibits its series phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21408156; PubMed-11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.; "C-jun N-terminal kinase (JNK)-interacting protein-lb/islet-brain-1 Scaffolds Alzheimer's amyloid precursor protein with JNK."; Neurosci. 21:6597-6607(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    processed in the Golgi complex.

DOMAIN: The NPXY sequence motif found in many tyrosine-
phosphorylated proteins is required for the specific binding of
the PID domain. However additional amino acids either N- or C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein. C-terminally'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                 MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurosci. 19:7507-7515(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH MAPKBIP1.
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terminal to the NPXY motif are often required for complete interaction. The NPXX site is also involved in clatherin-mediated
                                                                                                PTM: O-glycosylated.
MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
Ainc-binding increases heparin binding. No Cu(II) reducing activity with copper-binding.
SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00319; A4_INTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQUIRED FOR COPPER(II) REDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAG. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
                                           during neuronal
by caspase-3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y->G: REDUCED BINDING OF APBBL.
P -> PP (IN REF. 2).
56516DC3EA40E4B0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 1; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). COPPER-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMYLOID-LIKE PROTEIN 1.
C30 (BY SIMILARITY).
                                          cleaved by caspases
in vitro, at Asp-623
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1; Mismatches
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EMBL; BC021877; AAH21877.1; -
PIR; A46362; A46362.
HSSP; P05067; IMWP.
                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:88046; Aplp1.
InterPro; IPR001868; A4_APP.
Pfam: pF02177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOIDA.
SWART; SW00006; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.3%;
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233 GGRAEGGEDEEEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 GGOAEGAEDELEV 23
                                          PTM: Proteolytically
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                                                                                    PTM: N-glycosylated.
                                                           apoptosis. Cleaved,
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644
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464
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653 AA;
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Best Local Similarity
Matches 10; Conserv
                                endocytosis.
                                                                       similarity).
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554
641
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SIGNAL
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DOMAIN
TRANSMEM
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CARBOHYD
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RESULT 10 NKX1_BISB1 œ

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                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                      MEDLINE-98138491; PubMed-9478004;
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
"cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                     Bison bison (American bison).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
B-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sodium/potassium/calclum exchanger 1 (Na(+)/K(+)/Ca(2+)-
exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
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Vision; Transport; Antiport; Symport; Calcium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                        259 275 POTENTIAL.
218 242 POLY-GLU.
300 300 301 W. 2BES92DASAB9781E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Potassium transport; Sodium transport; Transmembrane
300 AA
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 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                   SEQUENCE FROM N.A.
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                                                                  SLC24AÎ OR NCKX1
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TRANSMEM
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SEQUENCE
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                          Ligase; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- COFACTOR: Binds 1 zince ion per subunit (By similarity).
-:- SUBUNIT: Homodimer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARIY: Belongs to class-I aminoacyl-tRNA synthetase family.
MetG subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; Prologo Melnologo Melnologo Melnologo Melnologo Melnologo Melnologo Metalogo M
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Q28139; 046384;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
exchange protein (Retinal rod Na-Ca+K exchanger).

SLC24A1 OR NCKXI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRNA-BINDING.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE010375; AAM02063.1; -.
HAMAP; MF_00098; fused; 1.
InterPro; IPR004495; MetG_Cterm.
InterPro; IPR001405; LRNA-synt_la.
InterPro; IPR002300; tRNA-synt_l.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002304; tRNA_bind.
Pfam: PF00133; tRNA_bind.
Pfam: PF00138; tRNA_bind.
Pfam: PF01588; tRNA_bind; 1.
Pfam: PF01588; MetRS_dimerising; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Pred. No.
MEDLINE-21927647; PubMed-11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77386 MW;
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53.3%;
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LLPEESGESEGODDE 561
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 AA;
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Conservative
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234 23
244 24
857 85
1216 AA;
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les 9; Conserv
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11179
11186
1207
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P41144;
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CONFLICT
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                      Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;

"CDNA cloning of the human retinal rod Na-Ca + K exchanger:

comparison with a revised bovine sequence.";

IL Invest. Ophthalmol. Vis. Sci. 33:435-440(1998).

-1- FUNCTION: Critical component of the visual transduction cascade,

controlling the calculum concentration of outer segments during

light and darkness. Light causes a rapid lowering of cytosolic

free calculum in the outer segment of both retinal rod and cone

photoreceptors and the light induced lowering of calculum is caused

by extrusion via this protein which plays a key role in the

process of light adaptation. Transports one Ca(2+) and one K(+) in

exchange for four Na(+) (By similarity).

-1- SUBCELDULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                           Primary structure and functional expression of the Na/Ca, K-exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: AC02564; AM88884.1; -.
PIR; S20969; S20969.
InterPro: IPR004817; K.NaCaexchang.
InterPro: IPR004817; K.NaCaexchang.
InterPro: IPR004837; NaCa_Exmemb.
Pfam; PF01699; Na_Ca_Ex; Z
TIGRFAMs; TIGR00367; ZA1904; 1.
TIGRFAMs; TIGR00367; TIGR00367; IIGR00367; IIGR0ADST; Antiport; Symport; Calcium transport; Potassium transport; Sodium transport; Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat; Alternative splicing.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SODIUM/POTASSIUM/CALCIUM EXCHANGER 1. EXTRACELLULAR (POTENTIAL).
                                                                                                        MEDLINE-92258377; PubMed-1582405;
Rellaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249; 647-660 AND 1119-1136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note-No experimental confirmation available;
--- TISSUE SPECIFICITY: Retina.
--- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                       SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=028139-2; Sequence=VSP_006159;
                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=028139-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                       from bovine rod photoreceptors.";
EMBO J. 11:1689-1695(1992).
                                                                                                                                                                                                    TISSUE-Retina;
MEDLINE-98138491; PubMed-9478004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X66481; CAA47108.1; -.
                                 Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
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                                                                                             rissuE-Retina;
                                                                                                                               200k N.J.;
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D-E-D-E-G-E-
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MEDLINE=94224825; PubMed=8170987;
Xie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T.,
Goldstein A., Watson S.J., Akil H.;
"Primary structure and functional expression of a guinea pig kappa opiold (dynorphin) receptor."
1 receptor."
1 receptor."
1 receptor."
1 receptor."
1 record Sci. U.S. A. 91:3779-3783(1994).
1 CN CURRENTS NEUROTRANISHITER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
MISSING (in isoform 2).
FTIG-VSP_006159.
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).

8 X 17 AA TANDEM REPEATS OF D-
I-Q-A-G-E-[GA]-G-E-V-[EK]-G.
1 (APPROXIMATE).
3.
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Pred. No. 44;
5; Mismatches 6; Indels
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PHOSPHORYLATION (POTENTIAL).
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131614 MW; 39F149A74D1D0523 CRC64;
                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Kappa-type opioid receptor (KOR-1).
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                                                                                                                                                                 POTENTIAL.
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ATP-binding;
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SEQUENCE
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09XT90;
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Matches
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                           PALMITATE (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-97086699; Pubwed-8932388;
Quigley F., Dao P., Cottet A., Mache R.;
"Sequence analysis of an 81 kb contig from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q38953; Q9LRVO;
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
AT3G26560 OR MFE16.8
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 1; Length 380;
                                                                                                                             PIR; ADSA29; ADSA29.
InterPro: IPR000276.
InterPro: IPR000276.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LAGWLRPEDGGQAEGAEDELE 22
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                                                                                                                                                                                                                                                                                                                                                                                                            42736 MW;
                                                                                                               EMBL; U04092; AAA67171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         38.1%;
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39
380 AA;
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                                                                                                                        PIR; A55259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                I. Sequence
                                                                                                                                                                                                            DNA Res. 7:131-135(2000).

-I- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Nuclear (Probable).

-I- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
SUBFAMILY. DOXA(FRP22 ORTHOLOG.

-I- SIMILARITY: Contains 15 morth domain.

-I- CAUTION: Ref.1 sequences differ from that shown due to a
frameshift in position 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                         features of the regions of 4,504,864 bp covered by sixty Pl and TAC
SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
STRAIN-EV. Columbia;
SEDIINE-20277480; PubMed-10819329;
Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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16-OCT-2001 (Rel. 40, Last sequence update).
28-FEB-2003 (Rel. 41, Last annotation update).
Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
(Membrane-type matrix metalloproteinase 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (WT1MMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1; Length 1168;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3632DE4A7A7690C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL) DEAH BOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002464; DEAH box.
InterPro; IPR001650; Helicase_C.
InterPro; IPR03029; S1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00271; helicase_C; 1.
SWART; SW00487; DEXDC; 1.
SWART; SW00480; HELICC; 1.
PROSITE; PS000560; DEAH_ATP_HELICASE; 1.
PROSITE; PS50126; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S1 MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X98130; CAA66825.1; ALT_FRAME.
EMBL; X97970; CAA66613.1; ALT_FRAME.
EMBL; BA028611; BAB01838.1; -.
HSSP; P05055; 1SRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 EDGDGMLYQEEGAEELEI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.8%;
57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarion
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1168 AA;
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ZINC (CATALTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
W; B782C2C569A96CAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R MEROPS; M10.014; -.

R InterPor; IPR000085; Hemopexin.

R InterPor; IPR0010818; Matrixin.

R InterPor; IPR0010818; Matrixin.

R InterPor; IPR006025; Zn_MTpeptdse.

R InterPor; IPR006025; Zn_MTpeptdse.

R Pfam; PF000413; Peptidase_M10_N; 1.

R Pfam; PF00133; Peptidase_M10_N; 1.

R PRINTS; PR00138; MATRIXIN.

R SMART; SM00120; HX; 4.

R RART; SM00120; HX; 4.

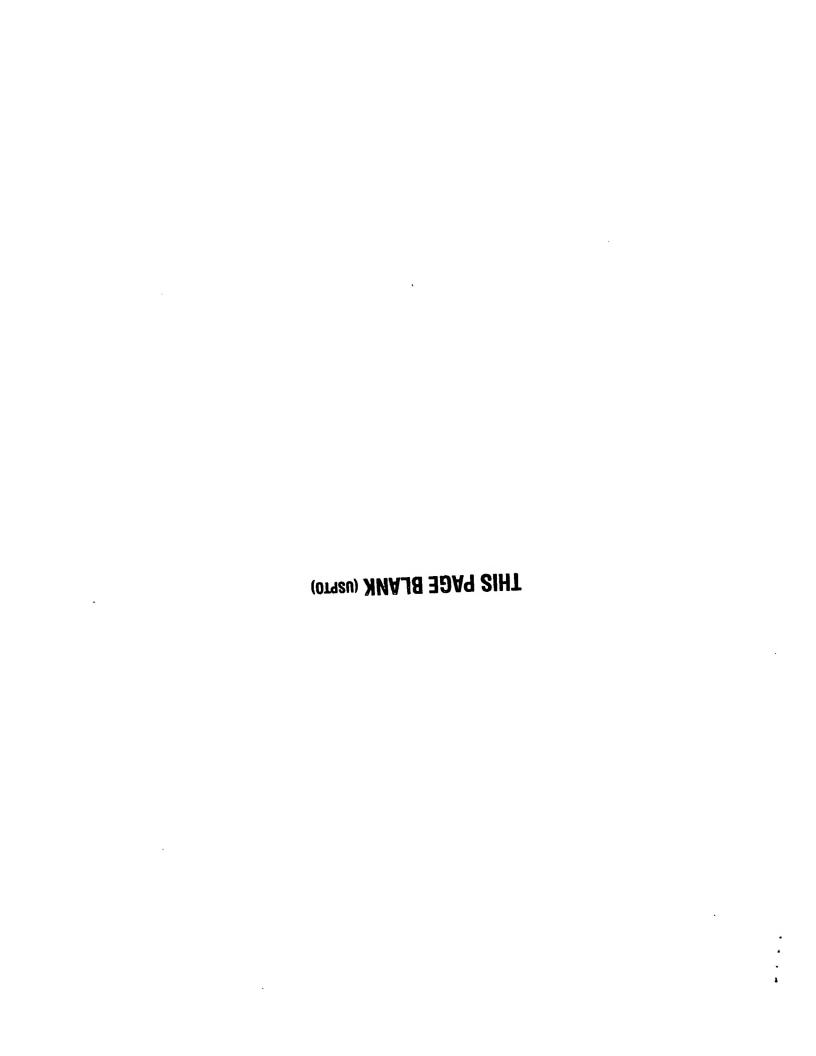
R PROSITE; PS00124; HEMOPEXIN; 1.

R PROSITE; PS00142; ZIMC; POTENSE; 1.

R PROSITE; PS00546; CYSTEINE_SWITCH; 1.

W HYDROLASE; Metalloprotease; Zinc; Zymogen; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.6%; Score 45.5; DB 1; Length 580; larity 45.8%; Pred. No. 48; Conservative 3; Mismatches 9; Indels
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MATRIX METALLOPROTEINASE-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                       MEDLINE-99095929; PubMed-9881602;
Caron C., Xue J., Bartlett J.D.;
"Expression and localization of membrane type 1 matrix
metalloproteinase in tooth tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). HEMOPEXIN-LIKE.
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MEROPS; M10.014; -.
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es 11; Conserv
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Matches
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Search completed: September 11, 2003, 17:21:44 Job time : 3.32086 secs



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08elh4 cocanobacil
081179 oryza sativ
07843 human immun
090p53 human immun
090n13 human immun
090n16 human immun
090n10 human immun
090n11 human immun
090n11 human immun
090n12 human immun
090n12 human immun
090p31 human immun
090p31 human immun
090p31 human immun
090p31 human immun
                      09077 human immun 090077 human immun 09177 human immun 081876 oryza sativ 089184 bos taurus 0901217 deinococcus 090085 human immun 09018 human immun 089192 pseudomonas 091282 pseudomonas 092282 pseudomonas
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            O9rv90 deinococcus
09rh77 bradyrhizob
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOd;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025791; AAR125791.1; -.
InterPro: IPR006737; motilin_assoc.
Interpro: IPR006738; motilin_assoc.
Ffam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                          Q8LI79
Q78494
Q90P53
Q90NL3
Q90NL6
Q90NL0
                                                                                                       Q90P55
Q90NK8
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090NM2
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Q943L4
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Q9GLE4
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Q9ETM8
                                                                                                                                                                                                  ОВЕГН4
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Q8CH53;
01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003) (TrEMBLrel. 23, 01-MAR-2003)
 PRELIMINARY;
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SEQUENCE FROM N.A.
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Matches
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Q8CH53
ID Q8CH
AC Q8CH
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DT 01-M
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Q8TAT9
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Q815t3 plasmodium
Q814t5 plasmodium
Q814t5 plasmodium
Q810p58 human immun
Q27724 plasmodium
Q90p50 human immun
Q91611 pseudomonas
Q91611 pseudomonas
Q91618 hirame rhab
Q9189 hirame rhab
Q95169 capra hircu
Q96189 capra hircu
Q9618 caenochabdi
Q8xw90 ralstonia s
Q8xw90 ralstonia s
Q80n15 human immun
Q8ufa5 agrobacteri
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                                                                                                     (without alignments)
271.100 Million cell updates/sec
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                                                                                      September 11, 2003, 17:21:03; Search time 21.893 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein – protein search, using sw model
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Q8LNL6
Q90P58
Q27724
Q90P50
Q916L1
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Q95169
Q95169
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Q90NL5
Q8UFA5
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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sp_archeap:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp_virus:*
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112...
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922
533
522
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523
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Perfect score:
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                                                                                        Run on:
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No.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5833;
            Plasmodium falciparum
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Hypothetical prot
                                                                                                                                   Organisms.";
                                                                                                East J.M.
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Best Local 5
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Paln A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Falinanb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                      Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
Ishii H.;
                                                                                                                               "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR442491; AA006655.1; - SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                     Meriones ungulculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59, DB 5; Length 1208;
Pred. No. 8.2;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                         76.0%; Score 92; DB 11; Length 11 llarity 73.9%; Pred. No. 1.3e-05; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE014846; AAN36207.1; -. SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                       | | | | | | | GWCRPKDNKTSDGYNDELE 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 48.8%; Similarity 52.6%; 10; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
P-type ATPase4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 419:498-511(2002).
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                        P-type ATPase, putative
           Ghrelin preproprotein.
                                                                                                                                                                                                     Local Similarity
es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                             SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=10047;
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Q9U445
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                                                                                                              "Expression and Functional Characterization of a Plasmodium falciparum
                                                                                                                                                                                          J. Biol. Chem. 276:10782-10787(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. Nipponbare;
McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
Kuit K., Nascimento L., Zutavern T., Ballja V., Ball M., Baker J.,
Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBAOO71120, from chromosome 10, complete sequence.";
Submitted (JUL-2002) to the BML/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                           Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
SEQUENCE FROM N.A.
MEDLINE-21179120; Pubmed-11145964;
Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 4.2;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO1494; ATPRSE_P-type; 5.
PROSITE; PS00154; ATPASE_E1_E2; 1.
ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SEQUENCE 1264 AA; 140261 MW; 638142BB1B433640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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183 AA; 20492 MW; DE73BD8607292D7B CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB:
Pred. No. 8.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 AA
                                                                                                                                                                                                                                                               EMBL, AFASES).

EMBL, AF203980; AAF17245.1; ..

HSSP; P04191; 1EUL.

InterPro; IPR001757; ATPase_E1-E2.

InterPro; IPR006068; Cation_ATPase_C.

- ----- IPR004014; Cation_ATPase_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00689; Cation_ATPsse_C; 1.
Pfam; PF00690; Cation_ATPasse_N; 1.
Pfam; PF00122; E1-E2_ATPasse; 1.
Pfam; PF00702; Hydrolasse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1128 GWCRPKDNKTSDGYNDELE 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%;
52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00119; CATATPASE.
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Best Local Similarity 47.6
Matches 10; Conservative
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF370919; AAK66318.1; -.
Interproy: IPR000777; GP120.
Pfam; PF0016; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%; Score 52; DB 15; Length 201;
45.5%; Pred. No. 13;
tive 3; Mismatches 9; Indels
                                                                                                                                43.8%; Score 53; DB 5; Length 1228; 50.0%; Pred. No. 61;
                                                                                                                                                                        6; Indels
                                  TIGRFAMS; TIGRO1494; ATPase_P-type; 5. PROSITE; PS00154; ATPASE_BIL_E3, 1. ATPASE_HILES; HORDINGS; HYDRO1898; Phosphorylation; Transmembrane. SEQUENCE 1228 AA; 135989 WW; 32C3CFD324964CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
22550 MW; 6CAF6C460A9BA517 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retrold viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                   201 AA
                                                                                                                                                      Pred. No. 61;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
                                                                                                                                                                                                               5 WLRPEDGGQAEGAEDELE 22
PRINTS; PR00119; CATATPASE.
                                                                                                                                                      Local Similarity 50.0 nes 9; Conservative
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hes · 10; Conservative
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201 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11676;
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SEQUENCE
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                                                                                                                                                                      Matches
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SO RE ROS
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-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dyer M., Jackson M., McWhinney C., Zhao G., Mikkelsen R.; "Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    "A Persistent Reservoir for HIV-1 in Alveolar Macrophages."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AR700911; AAK6510.1; -. Interpro; IPR00077; GP120. Pfam; PF00516; GP120; 1. AR60516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.8%; Score 53; DB 15; Length 202; Jarity 45.5%; Pred. No. 9.1; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 202
202 AA; 22572 MW; 4CBBACAFBFB14314 CRC64;
                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Envelope 91ycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Created)
01, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11676;
                                                                                                                                                      202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR006068; Cation_ATPase_C.
IPR004014; Cation_ATPase_N.
IPR005834; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LAGWLRPEDGGQAEGAEDELEV 23
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EMBL; 019298; AAC47167.1; -.
HSSP; P04191; 1EUL.
InterPro; IPR001757; ATPASE_E1-E2.
InterPro; IPR006068; Catton_ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00689; Cation_ATPase_C; 1.
Pfam: PF000690; Cation_ATPase_N; 1.
Pfam: PF00122; E1-E2_ATPase; 1.
Pfam: PF00702; HydroLase; 1.
                                          53 AGWIETEDGSDEESDESDESV 73
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                3 AGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
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                                                                                                                                                    PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
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Matches 10; Conserv
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Skeletal muscle voltage-gated chloride channel gClC-1 (Fragment).
Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE-97008165; Pubmed-8855341;
Beck C.L., Fahlke C., George A.L.;
"Molecular basis for decreased muscle chloride conductance in the
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                                                      Query Match 43.0%; Score 52; DB 12; Length 392; Best Local Similarity 75.0%; Pred. No. 26; Matches 9; Conservative 1; Mismatches 2; Indels
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SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;
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                Pfam; PF03216; Rhabdo_ncap_2; 1.
SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
F37D6.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         myotonic goat.";
Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
EMBL; UG0275; AAC48666.1; -.
InterPro; IPR001807; Cl-Channel_volt.
InterPro; IPR001807; Cl-Channel_volt.
PR00519; Sug_transporter.
Pfam; PF00571; CBS; 2.
Pfam; PF00554; voltage_CLC; 1.
                                                                                                                                                                                                              977 AA.
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67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0762; CLCHANNEL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
InterPro; IPR004902; Rhabdo_ncap_2.
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MEDLINE=99069613; Pubmed=9851916;
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                                                                                                                                 1111: || |||
378 EDGGEGEGGEDE 389
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                                                                                                                9 EDGGQAEGAEDE 20
                                                                                                                                                                                                                 PRELIMINARY;
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Q95169;
01-FEB-1997 (TrEMBLrel.
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nes 10; Conserv
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Best Local Si
Matches 10;
                                                          Query Match
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ID Q9N638
AC Q9N638;
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                                    REGULATORS.

EMBL. AE004466; AAG13668.1; -.

EMBL. AE004476; AAG13668.1; -.

Pfam: PF01022; HTH_ArsR.

PROMYS; PR00778; HTHARSR.

SMART; SM00418; HTH_ARSR.

SMART; SM00418; HTH_ARSR; 1.

DNA-binding; Transcription regulation; Complete proteome.

SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;
                                                                                                                                                                                 43.0%; Score 52; DB 16; Length 232; 72.7%; Pred. No. 15; 1: Indels 1; Indels
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 "Complete genome sequence of Pseudomonas aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Mononegavirales; Rhabdoviridae; Novirhabdovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Mononegavirales; Rhabdoviridae; Novirhabdovirus. NCBI_TaxID=38142;
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STRAIR=CA 9703;
OH H.K., Chol T.J.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104985; AAF14116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishizawa T.;
Nishizawa T.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D4542; BAA08261.1;
Interro; IPR004902; Rhabdo_ncap_2.
Pfam; PF03216; Rhabdo_ncap_2: 1:
PCam; PF03216; Rhabdo_ncap_2: 1.
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Last sequence update)
Last annotation update)
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Last annotation update)
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1-AUG-1998 (TrEMBLrel. 07,
1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Nucleocapsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111: || ||| |||
235 EDGGEGEGGEDE 246
                opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                Best_Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
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202 GWLRPQDGSRA 212
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                                                                                                                                                                                                                                          4 GWLRPEDGGQA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirame rhabdovirus
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01-AUG-1998
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082036
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SEQUENCE
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Rature 415.497-502(2002).

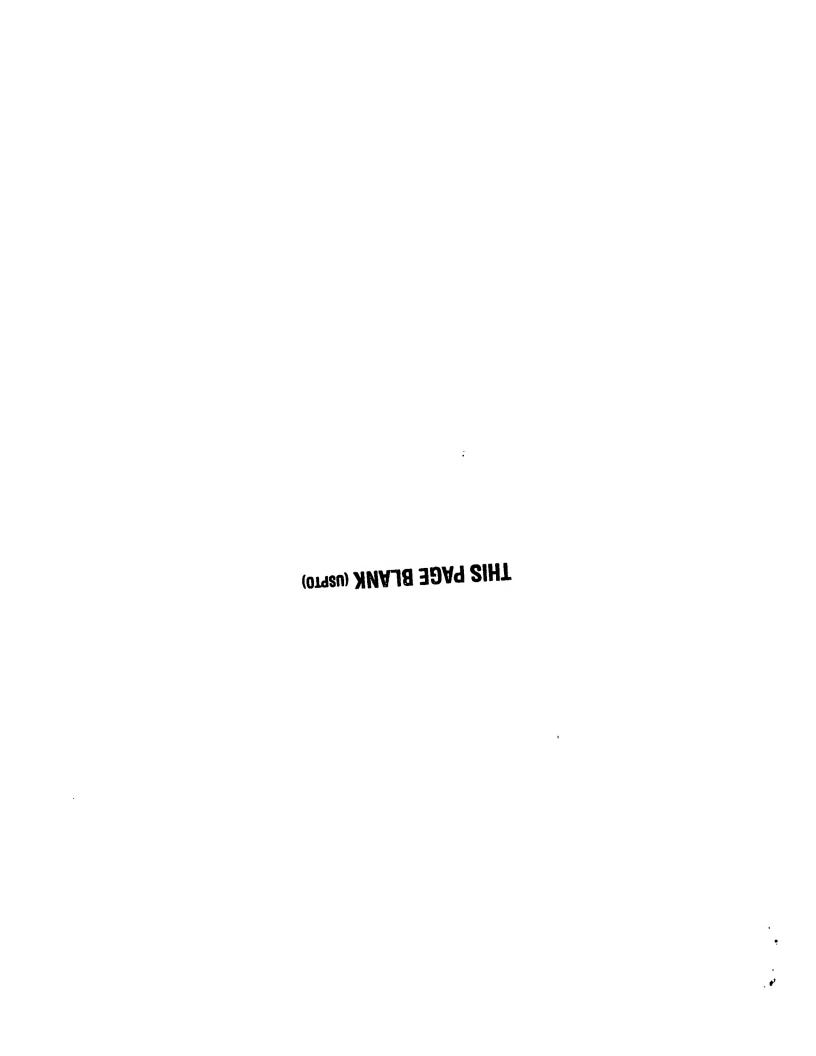
"EMBL; AL646070; CAD16292.1; -.

R Interpro: IRR001445; HTH_CopG.

R Pfam: PF004402; HTH_Chy J.

Hypothetical protein; Complete proteome.

SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria: Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51.5; DB 5; Length 436;
Pred. No. 34;
5; Mismatches 2; Indels
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                                                                                                                                                     McMurray A.A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 279600; CAB70221.1;
REMBL; 275540; CAB70221.1;
REMBL; 275540; CAB70215.1; JOINED.
REMBL; 275600; CAB70215.1; JOINED.
REMBL; 275600; CAB70215.1; JOINED.
ROTHEPPO; PF7006; CE24960.
R InterPro; IPR001132; Dwarfin.
R InterPro; IPR00132; Dwarfin.
R Pfam; PF03166; MH2; 1.
R SMART; SM00523; DWA; 1.
R SMART; SM00524; DWB; 1.
                         Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49496 MW; E0C71263BC580EEE CRC64;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last seq.
01-MAR-2003 (TrEMBLrel. 23, Last ann
Hypothetical protein RSc2585.
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MEDLINE-21681879; Pubmed-11823852;
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169 WIRPETNGGDDDGSEDK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                   investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA;
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Matches 10; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
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Q90NL5;
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Q90NL5
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September 11, 2003, 17:27:22 : Search time 24.2299 Seconds
(without alignments)
150.669 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human zsiq33-linke	Human zsig33-linke	Human exon 3-delet	Human des-Gln14-qh	Protein designated				
ID	AAE23840	AAE23841	AAE15885	AAE15886	AAE23839	AAE15884	AAE33410	AAB60517	AAW87991
DB	23	23	23	23	23	23	24	22	20
Length	23	23	23	23	24	24	91	116	111
% Query re Match Length DB II	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	23	23	23	23	23	23	23	23	23
Result No.	-	7	e	4	S	9	7	80	6

ALIGNMENTS

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Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                                                                                                                                                                       Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
                    AA.
                                                                               Human zsig33-linker peptide #2.
                    AAE23840 standard; peptide; 23
                                                                                                                                                                                                            10-MAY-2001; 2001US-0853253.
                                                                                                                                                                                                                                11-MAY-2000; 2000US-203300P.
                                                             10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                   (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
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                                                                                                                                                                  US2002055156-A1.
                                                                                                                                                Homo sapiens.
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RESULT 1
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          2SIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones .
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                                                                                          The invention relates to zsig33-like peptides and their corresponding
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE23841 standard; peptide; 23 AA.
                                                                Claim 1; Page 28; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zsig33-linker peptide #3.
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23; Conservative
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) SHEPPARD P O.
) DEISHER T A.
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Best Local 9
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(DEIS/)
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The invention relates to zaig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZiG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnosits assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZiG33 peptides are used as antigens in the production of antibodies against ZiG33 and in assays to identify modulators of ZiG33 expression and activity. The anti-ZiG33 antibodies are also used as diagnostic agents for detecting the presence of ZiG33 in samples (e.g. by enzyme linked immunosorbent assay (ELEA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and hormones, and/or secretion of digestive enzymes and hormones, and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide, zsig33-linker peptide.
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contractility, nutrient uptake, growth hormones and/or secretion of
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100.0%; Pred. No. 5.9e-15;
tive 0; Mismatches 0;
                                   digestive/pancreatic enzymes and hormones
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                                                                                                             Claim 1; Page 28; 34pp; English.
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Matches 23; Conservative
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N-PSDB; AAD25760.
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AAE15885
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Deisher TA, Bishop PD;

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The invention relates to zsig33-like peptides (zS33LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and czsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and czsig33-like peptides and nucleic acid molecules encoding such zsig33-like peptides. Zs33LP peptides actinvate the immune system in boosting immunity to infectious diseases, treating immunocompromised to patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, patients, in improving vaccines and in treatment of bacterial, viral, patients, in concern the invention and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption chhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and chromone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile clissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. Zs31zp peptides, nucleic acids and/or antibodies are useful for treating disorders as and/or braynes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker
                                                                                                                                                                                                                                                 New polypeptides, useful for modulating gastric contractility, nu uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises ssigi3-like peptides
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1c; Page 82; 89pp; English.
                                                                                              Jaspers SR, Sheppard PO,
                                (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; zsig33-like peptide; Zs33LP; immunity; developmental process;
infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
adsorption enhancer; gastrointestinal disease; growth related disease;
inflammation; gene therapy; growth regulation; blood vessel formation;
HIV; zsig33-linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                  invention relates to zsig33-like peptides (ZS33LP) including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                          Claim 1b; Page 81; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human zsig33-linker peptide #3.
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zsig33-like peptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23. AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001.
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Matches
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Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                          AAE23839 standard; peptide; 24 AA
                                                                                                                                                                                                                                                                                                                                                                                    Human zsig33-linker peptide #1.
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Gaps

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Indels

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Pred. No. 5.9e-15;

Mismatches,

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Homo sapiens.
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                                                                      Region
                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to zaig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assays (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide, zsig33-linker peptide.
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                                                                                                                                                                                                                                                                                                                                                   2SIG33-Like peptides and polynucleotides, useful for modulating gastric
contractility, nutrient uptake, growth hormones and/or secretion of
digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; zsig33-like peptide; Zs33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33-linker peptide.
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                                                                                                                                                                                                                                                                  Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 23;
100.0%; Pred. No. 6.1e-15;
Live 0; Mismatches 0;
/note= "Hydrophilic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE15884 standard; peptide; 24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 28; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zsig33-linker peptide #1.
                                                                                                     10-MAY-2001; 2001US-0853253
                                                                                                                                        11-MAY-2000; 2000US-203300P.
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                                                                                                                                                                                                                                                                Jaspers SR, Sheppard PO,
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                                                                                                                                                                         (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                                                                                                                 WPI; 2002-443750/47.
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es 23; Conserva
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                                                                    09-MAY-2002
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Matches
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The invention relates to zsigi3-like peptides (zSi3LP) including zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-like peptides and nucleic acid molecules encoding such zsigi3-like peptides. Zsi3LP peptides actid molecules encoding such casigi3-like peptides. Zsi3LP peptides actid molecules encoding such munoideficiency virus (HIV) patients, in improving vaccines and in treatment of beterial, viral, protocoal and fungal infections. Peptides of the invention are used to identify and cinclar receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption channers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These class are useful for treating disorders associated with one and/or call-cell interactions of tissues and contractile custom and contractine diseases. Zsizup peptides, nucleic are acids and/or antibodies are useful for treation of the astrointestinal and growth related diseases. Zsizup peptides, nucleic acids and contractions of diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides, useful for modulating gastric contractility, nu uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises ssig33-like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                     /note= "Hydrophilic antigenic site"
7..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deisher TA, Bishop PD;
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100.0%; Pred. No. 6.1e-15;
ive 0; Mismatches 0;
                                                                                                                                                                       /note- "Hydrophilic region"
Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2001; 2001WO-US15091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000; 2000US-0569271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jaspers SR, Sheppard PO,
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-082982/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD25760
                                                                                                                                                                                                                                                                    WO200187933-A2
                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001.
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in calls. The peptides are ghrelin homonogues and are concentration in calls. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth no accompanying side effects. The present sequence represents a chillin type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                            New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 186-187; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                            Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                    of infant growth disorders -
                                                                                                                   23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                               2000WO-JP04907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                            Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                               WPI; 2001-159704/16.
                                                                                                                                                                                                    (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAF59647
WO200107475-A1
                                                                               24-JUL-2000;
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                                       01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW87991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW8799
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                                                                                                                                                          Ghrelin; preproghrelin; GHS-R lb; benign prostatic hyperplasia; therapy; breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, and exon-3 deleted preproghrelin and/or a GHS-H lb proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghrelin and antagonists are useful for treating cancer of the reproductive system such as prostate, overlan, breast, cervical or uterine cancer, choricocarcinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 24; 100.0%; Pred. No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herington AC;
                                                                                                                     Human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60517 standard; Protein; 116 AA.
AAE33410 standard; Protein; 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins or nucleic acids
                                                                                                                                                                                                                                                                                                                                                             10-MAY-2002; 2002WO-AU00582.
                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2001; 2001AU-0004919.
17-DEC-2001; 2001AU-0009567.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-111957/10.
N-PSDB; AAD50726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AA;
                                                                                                                                                                                                                                                                               WO200290387-A1.
                                                                                                                                                                                                  cancer; human.
                                                                                                                                                                                                                                          Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                             02-APR-2003
                                                                                                                                                                                                                                                                                                                       14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chopin LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB60517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                       AAE33410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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25-JUN-1999;
                                                                                      11-DEC-1998;
                                                   26-JUN-1998;
                                                             31-JUL-1998;
01-OCT-1998;
 06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM38890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                        Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or alielit variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; noctropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psorlasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 20; Length 117; 100.0%; Pred. No. 2.3e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY87236 standard; Protein; 117 AA.
                                                98WO-US05620
                                                                       97US-0822897.
97US-0041102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                     Deisher TA, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                            WPI; 1999-070071/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
                                                                                                                                                                           N-PSDB; AAX04550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200000610-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
WO9842840-A1
                                                                                   24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2000
                                                23-MAR-1998;
                                                                         24-MAR-1997;
                       01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY87236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
AAY87236
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human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticincing anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neutroprotective, cardiovascular antimicrobial, nootropic, hepatotropic, neutroprotective, cardiovascular and antiasthamatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (Including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclarosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma. Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or diseases, schizophrenia, ovulatory defects, muscular dystrophy, HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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100.0%; Pred. No. 2.3e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 168-169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                            98US-0094983.
98US-0102686.
98US-0112129.
99WO-US14484
                                                                                          98US-0090762
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-160673/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ98121
                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akerblom IE,
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The invention relates to a method of forming a reversible peptider receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zaig33 peptide (Comprising residues 24-37 of AAB65649), where the receptor binds to the zaig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pencreatic enzymes and hormones, secretion of digestive and pencreatic enzymes and hormones, secretion of insulin-like growth factor i, secretion of non-zaig33 proteins. It is useful for modulating growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, protein catabolic responses atter surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety required and stated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zaig33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-I; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; G-protein coupled receptor.
                                                                                                                                                     /note- "specifically claimed fragment that binds to the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Forming reversible peptide receptor complex for purifying cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                          Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 22;
100.0%; Pred. No. 2.3e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 93-94; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                 2000WO-US32074.
                                                                                                                                                                                                                                                                                             99US-0166765.
                                                                                                                                                                                                                                                                                                                                                          Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-355879/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF83678
                                                                                                                                                                                                     WO200138355-A2
                                                                                                                                                                                                                                                                22-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                          Sheppard PO,
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                             22-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarian 23;
                                                                                                                                                                                                                                   31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                        Peptide
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Matches
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ID AAB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the encoded polypeptides (AAMA18213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, mutinity of disease, amyotrophic utilisation of the activity, chemoteactic/chemokinetic activity, chemoteactic/chemokinetic activity, haemostatic and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                          Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
umyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                        Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                      Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAGWLRPEDGGQAEGAEDELEV 74
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                                                                                                                                                                                                                                                                                                                                                      Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB62649 standard; Protein; 117
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100:0%;
                                                                                                                                                                                 2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0653450.
200US-0653450.
2000US-0653450.
2000US-0653450.
                                                                                                                                                     26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
 amyotrophic lateral
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                                                                                                                                                                                                                                                                                                                                                                                     Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                                                                                        Liu C,
Wang 2,
                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI58046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.N.S disorders
                                                                                        WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification.
                                                                                                                                                                                                                                             03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                           29-NOV-2000;
                                                              Homo saplens
                                                                                                                                                                                                                 09-JUL-2000;
                                                                                                                                                                                                                                   19-JUL-2000;
                                                                                                                                                                                     21-JAN-2000;
                                                                                                                                                                                                   25-APR-2000;
                                                                                                                        26-JUL-2001
                                leukaemia.
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Best Local 3
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Gaps

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Length 117; Indels 8

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are modified amino acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein
                        Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide compounds which induce growth hormone secretion elevate cell calcium concentrations, useful in treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 22;
100.0%; Pred. No. 2.3e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human zsig33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 182; 210pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB78319 standard; Protein; 117
                                                                                                                                                                                                                                                                                                           23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of infant growth disorders -
                                                                                                                                                                                                                                                               24-JUL-2000; 2000WO-JP04907
                                                                       growth hormone deficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention
                                                                                                                                                                    40200107475-A1
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-2002
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                                                                                                                                                                                                                   01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see Secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jedunum tissue. Modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying.
                                                                                          SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive anzymes, inducing growth hormone secretion or modulating destric embtving .
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                                                                                                                                                                                                                                                                                                                                                                                /label- SGIP_peptide
/note- "this peptide is claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                 24..117
/label- Mature_protein
24..34
/label- SGIP_peptide
                                                                                                                                                                                                                                                               /label- Signal_peptide
24..117
                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; 54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0345157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US18306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard PO, Jaspers SR,
23-APR-2001 (first entry)
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-123010/13.
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                                                                                                                                           cherapy; human.
                                                 Zsig33 protein.
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                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1999;
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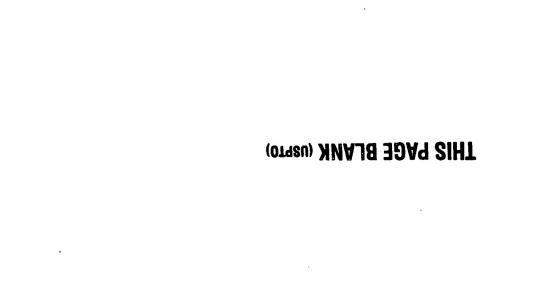
Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                        New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders
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100.0%; Score 23; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                  Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Columns 39-40; 23pp; English.
                           //note= "signal peptide"
24..119
/note= "mature protein"
Location/Qualifiers
                                                                                                                                                                                   30-JUN-2000; 2000US-0608810.
                                                                                                                                                                                                                        30-JUN-1999; 99US-141592P.
                                                                                                                                                                                                                                                                                                  Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                 WPI; 2002-634794/68.
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                                                                                                         US6420521-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
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 Key
Peptide
                                                      Protein
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Search completed: September 11, 2003, 17:51:55 Job time: 25.2299 secs

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4, Appli 22896, A 19, Appli 17695, A 2, Appli 1, Appli 1, Appli 1, Appli 1, Appli 10, Appl 20, Appl 20, Appl 20, Appli 20, App

Sednence Sed

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US-09-464-483-4
US-09-464-4
US-09-252-991A-2896
US-09-252-991A-17695
US-09-414-664-2
US-09-414-664-2
US-08-531-601-1
US-08-531-601-1
US-08-531-601-1
US-08-207-388-22
US-09-207-388-22
US-09-207-388-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Thereas A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98102
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: WA
                                                                                                                                                                                                                                                                                              US-09-046-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
 Sequence 2, Appli
Sequence 2, Appli
Sequence 268, Appl
Sequence 3033, Ap
Sequence 27033, Ap
Sequence 20368, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 612, Appl
Sequence 612, Appl
Sequence 26333, A
Sequence 26333, A
                                                                               September 11, 2003, 17:48:42; Search time 7.87166 Seconds (without alignments) 123.627 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                    1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-956-243-268
US-09-134-001C-3033
US-09-252-991A-27032
US-09-252-991A-16798
US-08-252-991A-16798
US-08-252-991A-16798
US-08-408-8520-31
US-08-408-8520-31
US-09-135-994-12
US-09-135-994-12
US-09-198-452A-612
US-09-198-452A-612
US-09-252-991A-32089
US-09-252-991A-32089
US-09-252-991A-32080
US-09-252-991A-32080
US-09-252-991A-3008
US-09-252-991A-3008
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                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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23
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Match Length
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Sequence:
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Gaps

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Length 117 Indels

Query Match 100.0%; Score 23; DB 3; 1 Best Local Similarity 100.0%; Pred. No. 2.8e-15; Matches 23; Conservative 0; Mismatches 0;

MOLECULE TYPE: protein FRAGMENT TYPE: internal

US-09-046-479-2

Sequence 1, Appli Sequence 18951, A

1, Appli 1, Appli

Sequence

Sequence 6794, Ap Sequence 33000, A Sequence 2, Appl1 Sequence 120, App Sequence 29569, A

US-09-266-965-120 US-09-252-991A-29569 -09-252-991A-33000 -09-328-352-6794

TOPOLOGY: linear

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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                           Length 117;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                           100.0%; Score 23; DB 4; 1
100.0%; Pred. No. 2.8e-15;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001.11-14

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1997-11-24

PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-04-28

PRIOR PLING DATE: 1998-04-28

PRIOR PLING DATE: 1998-04-28

PRIOR PRING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                         52 ALAGWLRPEDGGQAEGAEDELEV 74
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 23; Conservative
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                               ; NAME/KEY: SIGNAL
; LOCATION: (1) ...(23)
US-09-608-810A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-996-243-268
                                                                                        LENGTH: 117
TYPE: PRT
                                                                         SEQ ID NO 4
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTEM: DOS
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
FILLING DATE:
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
1 ALAGWLRPEDGGQAEGAEDELEV 23
                     52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                             Sequence 2, Application US/08822897C
Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SAWALBLAK, DEBOOTAN A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                        US-08-822-897C-2
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                                                                                          RESULT
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1998-05-07 NUMBER: 60/087106 1998-05-28 NUMBER: 60/087607 1998-06-02 NUMBER: 60/08759 1998-06-02 NUMBER: 60/087759 1998-06-03 NUMBER: 60/087827 1998-06-03 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088021		1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1
FILING DATE: APPLICATION FILING DATE: APPLICATION APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION AP	PPLICATION	PILLING DATE: APPLICATION PILLING DATE: APPLICATION FILLING DATE: APPL
PRIOR	PRIOR PRIOR	PRIOR

PRIOR APPLICATION NUMBER: 60/08961
PRIOR FILING DATE: 1938-06-17
PRIOR FILING DATE: 1938-06-18
PRIOR APPLICATION NUMBER: 60/08901
PRIOR PLING DATE: 1938-06-18
PRIOR PLING DATE: 1988-06-18
PRIOR PLING DATE: 1988-06-18
PRIOR FILING DATE: 1988-06-19
PRIOR FILING DATE: 1988-06-19
PRIOR FILING DATE: 1988-06-19
PRIOR PLING DATE: 1988-06-22
PRIOR APPLICATION NUMBER: 60/09025
PRIOR PLING DATE: 1988-06-22
PRIOR PLING DATE: 1988-06-22
PRIOR PLING DATE: 1988-06-22
PRIOR PLING DATE: 1988-06-23
PRIOR PLING DATE: 1988-06-23
PRIOR PLING DATE: 1988-06-23
PRIOR PLING DATE: 1988-06-23
PRIOR PLING DATE: 1988-06-24
PRIOR PLING DATE: 1988-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1988-06-25
PRIOR PLING DATE: 1988-06-26
PRIOR PLING DATE: 1988-07-00
PRIOR PLING DATE: 1988-07-00
PRIOR PLING DATE

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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PPLIAG DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
NINGER OF SEQ ID NOS: 33142
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MATC J. RUBERfield et al.
APPLICANT: MATC J. RUBERfield et al.
APPLICANT: MATC J. RUBERfield et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.4%; Score 7; DB 4
100.0%; Pred. No. 25;
ative 0; Mismatches
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100.0%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-16798
; Sequence 16798, Application US/09252991A
; Patent No. 6551795
                                                                                                         US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08428488; Patent No. 564894 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa US-09-252-991A-16798
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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22 DGGQAEG 28
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERAIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-108
PRIOR FILING DATE: 1997-108
PRIOR FILING DATE: 1997-108-14
PRIOR FILING DATE: 1997-108-14
SEQ ID NOS: 5674
SEQ ID NOS: 5674
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                             Length 117;
                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 552;
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                                                                                                                                      ch 100.0%; Score 23; DB 4; I Similarity 100.0%; Pred. No. 2.8e-15; 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 7; DB 4;
100.0%; Pred. No. 20;
11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 7; DB 4;
100.0%; Pred. No. 24;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-27032
; Sequence 27032, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3033, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Staphylococcus epidermidis
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR PPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.4
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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189 DGGQAEG 195
                                                                                                                                                              Best Local Similarity
Matches 23; Conserve
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US-09-134-001C-3033
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                                                                                                                                             Query Match
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APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides involved in The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                            E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 97;
                                                                                                                                            COUNTRY: USA
ZIP: .20005-315
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC-1993
PRIOR APPLICATION NUMBER: PC-1993
PRIOR APPLICATION NUMBER: PS-1993
ATTORNEY/AGENT INFORMATION:
NAME: MSYSTS, Kenneth J.
REGISTRATION NUMBER: 25.146
REFERENCE/DOCKET NUMBER: 25.146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION NUMBER: 03806.0054-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.1%; Score 6; DB 2;
100.0%; Pred. No. 49;
:1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/08510646B Patent No. 6077699
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Lacroix, Patricia
Thibaut, Denis
Zagorec, Monique
Debussche, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 97 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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ADDRESSEE: Finnegan,
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Blanch,
APPLICANT: Crouzet,
APPLICANT: Jacques,
APPLICANT: Lacroix,
APPLICANT: Lacroix,
APPLICANT: Thibaut,
                                            STREET: LSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sir
; TOPOLOGY: linear
US-08-403-852D-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 QAEGAE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QAEGAE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-510-646B-32
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
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NENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 39;
PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 30
; OTHER INFORMATION: /note- "Position 30 - Glu-NH2."
US-08-428-488-13
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: J-APR-1995
CLASSIFICATION: 514
ATTONNEY/AGENT INPORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/POCKET NUMBER: 26,254
RELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1
OTHER INFORMATION: /note- "Position 1 - H-Ser.
            STREET: P.O. Box 1404
CITY: Alexandria
STATE: Vireit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.1%; Score 6; DB 1;
100.0%; Pred. No. 22;
iive 0; Mismatches
                                                                                                                                                                                                                                  ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blanch, Veronique
Blanche, Francis
Crouzet, Joel
Jacques, Nathalle
Lacroix, Patricia
Thibaut, Denis
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Debussche, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 39
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100...
                                                                                                                                                                               STATE: Virginia COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GAEDEL 21
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US-08-403-852D-31
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GENERAL INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER ETLING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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100.0%; Pred. No. 49;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.1%; Score 6; DB 3
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches
                         FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTONEY, AGENT 1100-SMATION:
       US/08/403,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09135994A Patent No. 6280938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-135-994-12
                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 QAEGAE 18
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57 RPEDGG 62
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2 QAEGAE 7
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LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Debussche, Laurent
APPLICANT: Debussche, Laurent
APPLICANT: Decrey-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
          SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-A0G-1995
CLASSIFICATION NUMBER: US/08/510,646B
FILING DATE: 03-A0G-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
FILING DATE: 25-SEP-1993
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: ER 92/1146
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
FREIEFRANTION NUMBER: 03806.0054-01000
TELEFAN: (202) 408-4400
TELEFAN: (202) 408-400
TELEFAN: (202) 408-4000
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 6; DB 3. Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/231,818 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/09231818 Patent No. 6171846 GENERAL INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lacroix, Patricia
Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-510-6468-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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US-09-231-818-31
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Length 97;
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Sequence 12, Application US/09684843A

Sequence 12, Application US/09684843A

Sequence 12, Application US/09684843A

GENERAL NIVORMATION:
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE

FILE REFERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A

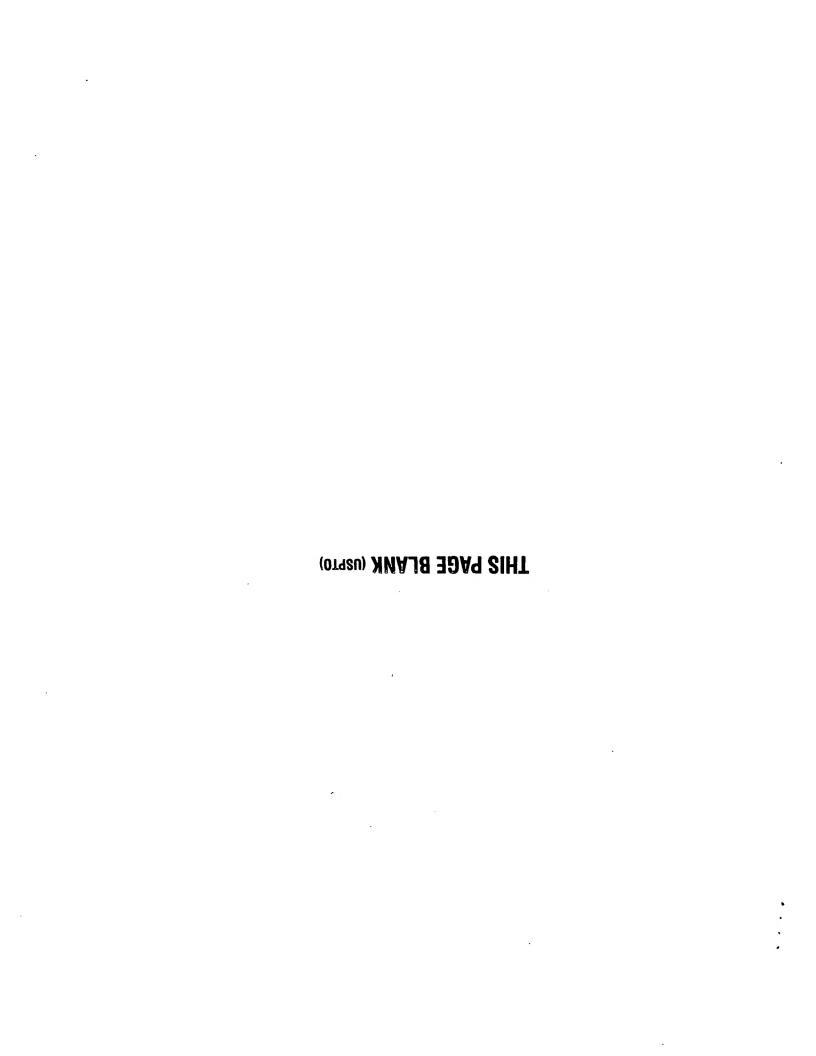
CURRENT APPLICATION NUMBER: 60/056,170

PRIOR APPLICATION NUMBER: 60/056,170

PRIOR APPLICATION NUMBER: 09/135,994
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RESULT 15
US-09-198-452A-612
US-09-198-452A-512
Sequence 612, Application US/09198452A
Factor No. 6559294
GENERAL INFORMATION:
APPLICANT: GTIffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
SEQ ID NOS: 6849
SEQ ID NOS: 6849
LENGTH: 183
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                                                                                                                                                                                              Length 129;
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                                                                                                                                                                                         Query Match 26.1%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 62; Matches 6; Conservative 0; Mismatches
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; PRIOR FILING DATE: 1998-08-18; NUMBER OF SEQ ID NOS: 14; SOFTWARE: PALENLIN VEr. 2.0; SEQ ID NO 12; LENGTH: 129; TYPE: PRT; ORGANISM: HOMO Saplens US-09-684-843A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-612
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57 RPEDGG 62
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US-09-990-456-268
US-09-989-721-268
US-09-989-293A-268
US-09-989-735-268
US-09-990-444-268
US-09-991-181-268
US-09-991-181-268
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US-09-990-562-268
US-09-990-711-268
US-09-989-726-268
                                                                                                                                                           US-09-990-436-268
US-09-993-687-268
US-09-989-734-268
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US-09-997-428-268
US-09-997-666-268
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US-09-990-437-268
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Facent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: SHEPPARD, PAUL
APPLICANT: BIESPARD, PAUL
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR PILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
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  RESULT 2
US-09-853-253-6
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US-09-853-253-5
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TYPE: PRT
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    SEQ ID NO 5
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Matches 2
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Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
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237.266 Million cell updates/sec
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                                                                                                                                       September 11, 2003, 17:55:57 ; Search time 14.1444 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-853-253-4
US-09-853-253-4
US-09-989-722-268
US-09-989-722-268
US-09-989-722-268
US-09-989-723-268
US-09-989-723-268
US-09-989-731-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
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US-09-991-073-268
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                                                                                                   OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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Word size

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Searched:

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Sequence

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Gaps

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Sequence 6, Application US/09853253; Patent No. US20020055156A1 GENERAL INFORMATION: APPLICANT: JASPERS, STEPHEN

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Result

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                                                                                                                                COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION ONDER: 09/046,479
FILING DATE: CUNKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: SAWISIBA, DEDOFAH A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2. Application US/09853253
Fatent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
APPLICANT: BISHOP, PAUL
APPLICANT: BISHOP, PAUL
FILE REFERENCE: 00-30
CURRENT APPLICATION: Zs1g33-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: 05/203,300
PRIOR PELING DATE: 2001-05-10
PRIOR PELICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: profesion
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                 COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
          CITY: Seattle
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US-09-853-253-2
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Pred. No. 9.4e-16;
Mismatches 0; Indels
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100.0%; Pred. No. 9e-16;
tive 0; Mismatches 0
APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
APPLICANT: BISHOP, PAUL
TILE OF INVENTION: ZS1933-11Ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT APPLICATION NUMBER: 60/203,300
PRIOR PILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, STEPHEN
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 284933-11ke Peptides
TITLE REFERENCE: 00-30
CURRENT FILLING DATE: 2001-05-10
PRIOR FILING DATE: 2000-05-11
NUMBER: OF SEQ ID NOS: 28
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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Patent No. US20020055156Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09794987 Patent No. US20010041791A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-853-253-4
                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
US-09-853-253-6
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R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
A APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
                                                                                     R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/08836

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088167

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/089742
R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08810
R APPLICATION NUMBER: 60/08824
R PILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08826
R APPLICATION NUMBER: 60/08826
R APPLICATION NUMBER: 60/088826
R APPLICATION NUMBER: 60/0888888
R RILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/089801

R RFILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089907

R APPLICATION NUMBER: 60/089908

R APPLICATION NUMBER: 60/089908

R APPLICATION NUMBER: 60/089948

R APPLICATION NUMBER: 60/089948

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089948

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089952

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089958

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089952

R APPLICATION NUMBER: 60/089952
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A APPLICATION NUMBER: 60/086217
R FILING DATE: 1998-06-05
R PILING DATE: 1998-06-09
R FILING DATE: 1998-06-09
R R PRICATION NUMBER: 60/08655
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R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-16
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089553
FILING DATE: 1998-06-17
                               FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/090254
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APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Walliam I.
APPLICANT: Long, Zemin I.
APPLICANT: Long, Zemin I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC63
CURRENT APLICATION NUMBER: US/09/989,722
CURRENT PILING DATE: 2001-11-19
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR APPLICATION NUMBER: 60/08/106
PRIOR PILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/08/767
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08/759
52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                               Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088025
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
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APPLICANT: Standy, Zealn
APPLICANT: Standy, Zealn
APPLICANT: Standy, Zealn
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: 05/04/987
PRIOR PLILNG DATE: 2001-11-19
PRIOR PADILOCATION NUMBER: 05/06/250
PRIOR PLILNG DATE: 1997-10-17
PRIOR PLILNG DATE: 1997-10-17
PRIOR PRIOR PADILOCATION NUMBER: 60/06/5311
PRIOR PLILNG DATE: 1997-10-17
PRIOR PRIOR PADILOCATION NUMBER: 60/06/5311
PRIOR PADILOCATION NUMBER: 60/06/5311
PRIOR PADILOCATION NUMBER: 60/06/530
PRIOR PLILNG DATE: 1997-10-12
PRIOR PADILOCATION NUMBER: 60/08/600
PRIOR PLILNG DATE: 1998-10-12
PRIOR PLILOCATION NUMBER: 60/08/20
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Fong, Sherman
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Goddard, Audrey
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Kljavin, Ivar J.
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              Ashkenazi,Avi J.
Baker,Kevin P.
Botstein,David
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                                                                                        Desnoyers, Luc
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                                                                                                                Eaton, Dan L.
GENERAL INFORMATION:
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100.0%; Pred. No. 3.5e-15;
tive 0; Mismatches 0;
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

RR FILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090472

R FILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/09035

RR APPLICATION NUMBER: 60/090536

RR APPLICATION NUMBER: 60/090540

RR APPLICATION NUMBER: 60/090540

RR APPLICATION NUMBER: 60/090540
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R FILING DATE: 1998-06-26
R PELICATION NUMBER: 60/091360
R PELING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R APPLICATION NUMBER: 60/091544
R APPLICATION NUMBER: 60/091544
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US-09-989-723-268
; Sequence 268, Application US/09989723
; Patent No. US20020072092A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
FILING DATE: 1998-06-25
FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
                60/090349
                                                              APPLICATION NUMBER: 60/090355
                                                                                                         APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
                                                                                                                                                                                                   APPLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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                APPLICATION NUMBER: 60/
FILING DATE: 1998-06-23
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Query Match Best Local S: Matches 23,

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PRIOR APPLICATION NUMBER: 60/08305
PRIOR APPLICATION NUMBER: 60/08302
PRIOR APPLICATION NUMBER: 60/08312
PRIOR APPLICATION NUMBER: 60/08312
PRIOR PELLING DATE: 1989-66-05
PRIOR APPLICATION NUMBER: 60/08313
PRIOR PILING DATE: 1989-66-05
PRIOR PELLING DATE: 1989-66-05
PRIOR PELLING DATE: 1989-66-10
PRIOR PILING DATE: 1989-66-10
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PRIOR APPLICATION NUMBER: 60/08810
PRIOR PELLING DATE: 1989-66-10
PRIOR APPLICATION NUMBER: 60/08816
PRIOR PILING DATE: 1989-66-10
PRIOR PELLING DATE: 1998-66-10
PRIOR PELLING DATE: 1998-6
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Gaps ö Length 117; Indels 100.0%; Score 23; DB 9; I llarity 100.0%; Pred. No. 3.5e-15; Conservative 0; Mismatches 0; Sequence 268, Application US/09989279; Sequence 268, Application US/09989279; Patent No. US20020072496A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Betstein, David; APPLICANT: Desnoyers, Luc; APPLICANT: Eaton, Dan L.; APPLICANT: Ferrara, Napoleone R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091360

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-02

R R FILING DATE: 1998-07-02

R R FILING DATE: 1998-07-02

R R FILING DATE: 1998-07-01 R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090444

R FILING DATE: 1998-06-24

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R FILING DATE: 1998-06-24

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R APPLICATION NUMBER: 60/090535

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R PILING DATE: 1998-06-24 R FILING DATE: 1998-06-24

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R APPLICATION NUMBER: 60/090678

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R APPLICATION NUMBER: 60/090694

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R APPLICATION NUMBER: 60/091978

R FILING DATE: 1998-07-07

R APPLICATION NUMBER: 60/091982

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R APPLICATION NUMBER: 60/092182

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APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633 FILING DATE: 1998-06-24
APPLICATION UNMBER: 60/090542
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557 Query Match Best Local Similarity Matches 23; Conserva US-09-989-279-268 22 PRIOR
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RAPPLICATION NUMBER: 60/089599
RETLING DATE: 1998-66-17
RAPPLICATION NUMBER: 60/089600
RETLING DATE: 1998-66-17
RAPPLICATION NUMBER: 60/089653
RETLING DATE: 1998-66-17
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RETLING DATE: 1998-66-18
RETLING DATE: 1998-66-18
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RETLING DATE: 1998-66-18
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RETLING DATE: 1998-66-18
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RETLING DATE: 1998-66-18
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RAPPLICATION NUMBER: 60/089948
RETLING DATE: 1998-66-19
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
A PAPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
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R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089440
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R FILING DATE: 1998-06-15
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R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
PILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
APPLICATION NUMBER: 60/090349
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APPLICATION UNBER: 60/090355
FILING DATE: 1998-06-29
APPLICATION UNBER: 60/090429
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APPLICATION UNMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090431
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989, 279
CURRENT APPLICATION NUMBER: G0/049787
PRIOR APPLICATION NUMBER: 60/049787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-13

R PELICATION NUMBER: 60/06670

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/075945

R RILING DATE: 1998-02-25

R APPLICATION NUMBER: 60/078910

R FILING DATE: 1998-04-28

R APPLICATION NUMBER: 60/08332

R APPLICATION NUMBER: 60/08332

R APPLICATION NUMBER: 60/08332

R APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07
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RETLING DATE: 1998-05-28

RETLING DATE: 1998-06-02

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RETLING DATE: 1998-06-03

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RETLING DATE: 1998-06-03

RETLING DATE: 1998-06-03

RETLING DATE: 1998-06-03

RETLING DATE: 1998-06-04

RETLING DATE: 1998-06-07

RETRING DATE: 1998
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                                                                                                        Grimaldi, J. Christopher
                                                                                                                                                                                                        Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K.
Williams, P. Mickey
  Gerber, Hanspeter
Gerritsen, Mary E.
                                                                             Godowski, Paul J.
                                                                                                                             Gurney, Austin L.
Kljavin, Ivar J.
                                                     Goddard, Audrey
                                                                                                                                                                                  Napier, Mary A.
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1998-06-24

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APPLICANT: Zhang, Zhang, Zhanim 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same PRINCE TRANSCORPE: 1937-06-16

PRIOR PELICATION NUMBER: 60/06250

PRIOR PELICATION NUMBER: 60/065311

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PRIOR PALICATION NUMBER: 60/065311

PRIOR PALICATION NUMBER: 60/08312

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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
                                                                                                                                                   Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                        Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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     Napler, Mary A.
                                                                                                                                             Daniel
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PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
DR PELING DATE: 1998-06-24

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DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090540

DR APPLICATION NUMBER: 60/090557

DR FILING DATE: 1998-06-24

DR PILING DATE: 1998-06-24

DR PILING DATE: 1998-06-26

DR PILING DATE: 1998-06-26

DR PILING DATE: 1998-06-25

DR PILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25

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R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-26

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R FILING DATE: 1998-07-01
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Patent No. US20020072497A1
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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Ferrara, Napoleone
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APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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Matches 23; Conserv
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PRIOR APPLICATION UNDERS: 60/08810
PRIOR PELING DATE: 1998-06-10
PRIOR PELICATION UNDERS: 60/08826
PRIOR PELICATION UNDERS: 60/08826
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PRIOR PELICATION UNDERS: 60/08826
PRIOR PELICATION UNDERS: 60/08810
PRIOR PELICATION UNDERS: 60/08910
PRIOR PELING DATE: 1998-66-19
PRIOR PELING DATE: 1998-66-19
PRIOR PELICATION UNDERS: 60/08910
PRIOR PELING DATE: 1998-66-19
PRIOR PELICATION UNDERS: 60/08910
PRIOR PELING DATE: 1998-66-19
PRIOR PELICATION UNDERS: 60/09013
PRIOR PELING DATE: 1998-66-19
PRIOR PELING DATE: 1998-66-19
PRIOR PELING DATE: 1998-66-19
PRIOR PELING DATE: 1998-66-19
PRIOR PELICATION UNDERS: 60/09013
PRIOR PELING DATE: 1998-66-20
PRIOR PELICATION UNDERS: 60/09013
PRIOR PELICATION UNDERS: 60
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| PRIOR APPLICATION NUMBER: 60/09054
| PRIOR PLILIC DATE: 1996-06-24
| PRIOR PLILIC DATE: 1996-06-24
| PRIOR PLILIC DATE: 1996-06-24
| PRIOR PLILIC DATE: 1996-06-25
| PRIOR PLILIC DATE: 1996-06-26
| PRIOR PLILIC DATE: 1996-07-01
| PRIOR PLILICATION NUMBER: 60/09154
| PRIOR PLILIC DATE: 1996-07-01
| PRIOR PLILIC DATE: 1996-07-02
| PRIOR PLILIC DATE: 1996-07-03
| PRIOR PLILICATION NUMBER: 60/09182
| PRIOR PLILICATION NUMBER: 60/09182
| PRIOR PLILICATION NUMBER: 60/09182
| PRIOR PLILICATION NU

Sequence 268, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P. Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Ferrara, Napoleone Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Kljavin, Ivar J. Napier, Mary A. Baker, Kevin P. Botstein, David Goddard, Audrey Desnoyers, Luc Eaton, Dan L. Pan, James US-09-989-731-268 APPLICANT: APPLICANT APPLICANT APPLICANT

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R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
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R APPLICATION NUMBER: 60/089948
R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090246
R APPLICATION NUMBER: 60/090246
R APPLICATION NUMBER: 60/090252
R RAPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
R R PILING DATE: 1998-06-24
R R PRILICATION NUMBER: 60/090445
R R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090472
R R PILING DATE: 1998-06-24
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R R APPLICATION NUMBER: 60/090472
                                                            R APPLICATION NUMBER: 60/08861

R APPLICATION NUMBER: 60/08861

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-12

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089105

R APPLICATION NUMBER: 60/089105

R APPLICATION NUMBER: 60/08912

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08958

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08958

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

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R APPLICATION NUMBER: 60/08959
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090678
60/088826
                                             APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/090542
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                     Williams, P. Mickey
Wood, William I.
Watanabe, Colin K
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/989,732 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787
                                                                                 PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-28
PRIOR PILING DATE: 1998-03-28
PRIOR PILING DATE: 1998-03-28
PRIOR APPLICATION NUMBER: 60/08760
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PRIOR PILING DATE: 1998-06-03
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C57
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100.0%; Pred. No. 3.5e-15;
ive 0; Mismatches 0;
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DR APPLICATION NUMBER: 60/090695

DR FILING DATE: 1998-06-25

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DR FILING DATE: 1998-06-25

DR PLING DATE: 1998-06-26

DR PLING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/090863

DR APPLICATION NUMBER: 60/090863

DR PILING DATE: 1998-06-26

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DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR FILING DATE: 1998-07-01
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DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091626

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02
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Patent No. US20020123463A1
GENERAL INFORMATION:
                             APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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   FILING DATE: 1998-06-25
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Goddard, Audrey
Godowski, Paul J.
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
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Best Local Similarity 100.
Matches 23; Conservative
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Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
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PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-19
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1018:
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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Best Local Similarity 100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0;
                            THE APPLICATION NUMBER: 00/050002

THE APPLICATION NUMBER: 60/090863

THING DATE: 1998-06-26

THING DATE: 1998-07-01

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Patent No. US20020127556A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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FILING DATE: 1998-07-07
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 FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090862
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Williams, P. Mickey
Wood, William I.
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Napier,Mary A.
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION UNDBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186

APPLICATION NUMBER: 60/049787

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	NUMBER: 60/08760 1998-06-02 1998-06-02 1998-06-02 1998-06-03 1998-06-03 1998-06-03 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08812 1998-06-04 NUMBER: 60/08812 1998-06-04 NUMBER: 60/08812 1998-06-04 NUMBER: 60/08812	NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06
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PRIOR PELICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-17
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PRIOR PILING DATE: 1998-06-19
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PRIOR PILING DATE: 1998-06-22
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PRIOR PILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R PILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538
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R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-10
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FILLING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/097607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/097609
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APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-05
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APPLICATION UNMBER: 60/088734
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/088655
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APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliam I.
APPLICANT: Sang, Zemin
TITLE OF INVEWTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVEWTION: Acids Encoding the Same
TITLE OF INVEWTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG8
CURRENT FILING DATE: 2001-11-14
PRIOR PLICATION NUMBER: 00/049787
PRIOR PLILNG DATE: 1997-06-16
PRIOR PRILNG DATE: 1997-10-17
PRIOR PLILNG DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR PLILNG DATE: 1997-11-24
PRIOR PLILNG DATE: 1998-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 10; 100.0%; Pred. No. 3.5e-15;
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091637
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 268, Application US/09990442 Patent No. USS/02013252A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity 100.0
Matches 23; Conservative
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Eaton, Dan L.
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US-09-990-442-268
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APPLICANT:
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R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
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R PILING DATE: 1998-06-18
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R PELING DATE: 1998-06-18
R PELING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
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R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-32
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090557
R PILING DATE: 1998-06-24
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R FILING DATE: 1998-06-25
A PAPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090695
R FILING DATE: 1998-06-28
R FILING DATE: 1998-06-28
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-26
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273/0PtC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR PILING DATE: 1998-05-03-20
PRIOR PILING DATE: 1998-05-03-20
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084500
PRIOR PILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/09182
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Napier, Mary A.
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Eaton, Dan L.
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APPLICANT:
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PRIOR PILLING DATE: 1998 06-02
PRIOR PILLING DATE: 1998 06-02
PRIOR PILLING DATE: 1998 06-03
PRIOR APPLICATION NUMBER: 60/08759
PRIOR APPLICATION NUMBER: 60/08727
PRIOR APPLICATION NUMBER: 60/08023
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PRIOR PILLING DATE: 1998 06-03
PRIOR PILLING DATE: 1998 06-04
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PRIOR PILLING DATE: 1998 06-04
PRIOR PILLING DATE: 1998 06-04
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PRIOR FILING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/08908
PRIOR PELICATION NUMBER: 60/08908
PRIOR PELING DATE: 1998-06-19
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PRIOR PELING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-06-25
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PRIOR PELICATION NUMBER: 60/090695
PRIOR PELICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-26
PRIOR PELICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-07-01
PRIOR PELICATION NUMBER: 60/090695
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PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
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PRIOR PELICATION NUMBER: 60/0901539
PRIOR PELING DATE: 1998-07-02
PRIOR PELICATION NUMBER: 60/0901539
PRIOR PELING DATE: 1998-07-02
PRIOR

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DR APPLICATION NUMBER: 60/08212

DR FILING DATE: 1998-06-05

BR FILING DATE: 1998-06-05

DR FILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088655

DR FILING DATE: 1998-06-09

DR FILING DATE: 1998-06-10

DR FILING DATE: 1998-06-10

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088738

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088742

DR FILING DATE: 1998-06-10

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R APPLICATION NUMBER: 60/088824

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R RPLICATION NUMBER: 60/088826

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/08861

R FILING DATE: 1998-06-11

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R APPLICATION NUMBER: 60/089513

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08958

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R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
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                          FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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FILLING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-04
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                                                                                                                   Length 117;
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Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1997-10-17
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PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/06770
PRIOR APPLICATION NUMBER: 60/06770
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PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-05-07
                                                                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                               Sequence 268, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker. Kevin P.
APPLICANT: Botstein, David
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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Grimaldi, J. Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Gerritsen, Mary E.
Goddard, Audrey
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Kljavin, Ivar J.
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Eaton, Dan L.
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US-09-993-604-268
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PRIOR PLING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089348
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PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090246
PRIOR PLING DATE: 1998-06-24
PRIOR PRIOR APPLICATION NUMBER: 60/09044
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09054
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09054
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09054
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09056
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-26
PRIOR PRILICATION NUMBER: 60/09164
PRIOR PRILICATION NUMBER:
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Search completed: September 11, 2003, 18:16:19 Job time : 15.1444 secs

Ouery Match
100.0%; Score 23; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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(without alignments)
253.289 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                          OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. piri:* pir2:* pir3:* PIR_76:* Database :

Post-processing: Listing first 45 summaries

quiescence specifi hypothetical prote hypothetical prote imidazolegiycerol-HL-60-induced diff diutamate transpor catechol 1,2-dioxy probable hydrogena conserved hypothet probable phosphogl hypothetical prote hypothetical prote corticotropin / li tropomyosin I, tho tropomyosin I, emb PD-1 protein - hum lipoprotein mtsA, hypothetical prote hypothetical prote hypothetical prote hypothetical prote transcription regu aconitate hydratas BOLF1 protein - hu cold-shock domain conserved hypothet ghrelin precursor probable membrane Description SUMMARIES D69070 A40866 T30002 A95298 A48990 B83451 QQBE10 C87574 AB0401 E82118 A30230 T46695 A91082 B85927 T48871 F72508 CTPGP r48894 Query Match Length DB Result

hypothetical protein F4D11.80 - Arabidopsis thaliana (C.;Species: Arabidopsis thaliana (mouse-ear cress) (C.;Species: Arabidopsis thaliana (mouse-ear cress) (C.;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 (C.;Accession: T04453 (C.;Accession: T04453 (C.;Accession: T04453 (C.;Accession: T04653 (C.;Accession: T04653 (C.;Accession: T0453 (C.;Accession: A.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hohelsel, J.; Mewes, submitted to the Protein Sequence Database, April 1998

A;Map position: 4 A;Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

A,Accession: T04453
A,Molecule type: DNA
A,Residues: 1-483 <BEV>
A,Cross-references: EMBL:AL022537
A,Experimental source: cultivar Columbia; BAC clone F4D11
C,Genetics:

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		226.1 226.1 226.1 226.1 226.1 226.1 226.1 226.1 226.1 226.1	3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	наааааааааааааа	E69690 735063 A83526 A83526 AE3323 AE3323 AD2697 G97314 AD2697 DCBSPR DCBSPR T24004 AF3321 AF3333	transcription repr JOS ribosomal prot probable prolipopr hypothetical prote sam-dependent meth cysteine proteinas cysteine proteinas hypothetical prote alcohol dehydrogen cysteine proteinas phosphoribosylamin molybdopterin bios hypothetical prote hypothetical prote hypothetical prote
					ALIGNMENTS	
RESULT 1 A59316 ghrelin precursor - human Ghalternate names: preproghrelin C; Alternate names: preproghrelin C; Species: Homo sapiens (man) C; Date: 16-Jun-2000 #sequence_revischess: Homo sapians C; Date: 16-Jun-2000 C; Maccession: A59316 A; Title: Ghrelin is a growth-hormor A; Retenence number: A59316; MUID:20 A; Catus: not compared with concept A; Molecule type: mRNA A; Residues: 1-117 < KGUJ> A; Cromment: Greences: GB:AB029434; NI A; Experimental source: tissue stome A; Note: submitted to GenBank, June C; Comment: Ghrelin secreted by the C; Comment: Ghrelin secreted by the C; Comment: Signal sequence #StE F; 1-23/Domain: signal sequence #StE F; 24-51/Product: ghrelin #status pp F; 24-51/Product: ghrelin #status pp F; 25-117/Domain: carboxyl-terminal F; 26/Binding site: octanoate (Ser) Query Match Matches 23; Conservative 0	precursor - hum ate names: prep s: Homo sapiens s: Homo sapiens s: Homo sapiens s: Homo sapiens divided hims and since number: A59 ion: A59316 since number and sources: GB: Abrances: GB: Abrances: GB: Abrances: GB: Abrances: GB: Abrances: GB: Abrances: Abr	unsor - human names: prepror nn - 2000 #sequ A5316 H59316 H59316 H59316 H59316 H59316: a gro liln is a gro number: A59316: compared wi F-17 (A0A) F-17 (A0A) F-17 (A0A) F-17 (A0A) F-17 (A0A) F-17 (A0A) F-17 (A0A) F-17 (A0A) I source: ti tted to GenB Nource: ti tted to Ge	sor - human mes: preproghrelin o sapiens (man) -2000 #sequence_revision 59316 6-660, 1999 in is a growth-hormone- in is a growth-hormone- spaie compared with conceptua compared with conceptua 117 < kGU> nces: GB: ABO29434; NID: source: tissue stomach ted to GenBank, June 19 elin secreted by the stu motilin motilin secreted by the stu inces: lipoprotein; sto slynal sequence #statu trannone; lipoprotein; sto	hrelin nce_revis Date, Y.; th-hormon ; MUID:20 h concept concept sue stoma nk, June d by the d by the rotein; s ence #sta status pr rotein; s ence #sta status pr rotein; d for (Ser)	sion 16-Jun-2000 #text Nakazato, M.; Matsuc ne-releasing acylated 3067959; PMID:10604470 cual translation 1999 stomach stimulates th stomach tus predicted <sig> redicted <art> redicted <art> propeptide #status pr (covalent) #status ex Score 23; DB 1; Len Pred. No. 4.1e-16; mismatches 0; I</art></art></sig>	000 #text_change 21-Jul-2000 .; Matsuo, H.; Kangawa, K. acylated peptide from stomach. :10604470 ion bibw:BAA89371.1; PID:g6691572 cells ulates the release of somatotropin (g. cells status predicted <ctp> status predicted <ctp> status experimental B 1; Length 117; 1e-16; 0; Indels 0; Gaps 0;</ctp></ctp>
Dp	 	IIIII Swlrpe		GAE	 DELEV 74	

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Gaps

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-910 <STO.
A;Cross-references: GB:AE004584; GB:AE004091; NID:g9947516; PIDN:AAG04951.1; GSPDB:GN
A;Experimental source: strain PAOl
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: C87574
R;Merman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A43041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1239 <BAN>
A;Cross-references: BMBL:V01555; NID:959074; PIDN:CAA24841.1; PID:91334855
R;Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Glbson, T.J.
Nature 310, 207-211, 1984
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
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A;Residues: 1-69 <S:TO>
A;Residues: 1-69 <S:TO>
A;Crosz-references: GB:AE005673; NID:g13424199; PIDN:AAK24591.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Sate: 25-Feb-1985 % sequence_revision 25-Feb-1985 % text_change 16-Jul-1999
C:Accession: A43041; A03752; S32995
C:Accession: A43041; A03752; S32995
Mol. Biol. Med. 1, 21-45, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BOLEI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cold-shock domain family protein (imported) - Caulobacter crescentus
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C;Superfamily: iron-responsive element-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 30.4%; Score 7; DB 2 Similarity 100.0%; Pred. No. 26; 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.4%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
                                 .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Status: preliminary
                                                                                                                                                                  A; Accession: B83451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           Dypothetical protein - Streptomyces lividans (fragment)

C;Species: Streptomyces lividans
C;Species: Streptomyces lividans
C;Species: Streptomyces lividans
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999
C;Accession: JH0572
R;Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;
R;Lichenstein, H.S.; Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.;
A;Title: Cloning and characterization of a gene encoding extracellular metalloprotease f A;Reference number: JH0571; MUID:92192468; PMID:1547948
A;Recession: JH0572
A;Residues: 1-302 < LLC>
A;Cossion: JH0572
A;Molecule type: DNA
A;Residues: GB:M89476; NID:g153411; PIDN:AAA26804.1; PID:g153412
A;Rosidues: Language the codon GTA for residue 260 as Asp
A;Note: the authors translated the codon GTA for residue 260 as Asp
A;Note: this protein has a strong similarity to Lysk family of transcriptional regulator
C;Superfamily: Pseudomonas putida regulatory protein catR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription regulator LysR family homolog SnpR - Streptomyces lividans C; Species: Streptomyces lividans C; Species: Streptomyces lividans C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change ll-Jan-2000 C; Accession: A48990
B; Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
A; Microbiol. 38, 912-920, 1992
A; Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid A; Reference number: A48990; MUID: 93099553; PMID: 1464066
A; Accession: A48990
A; Status: preliminary
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Molecule type: acide from NCBI backbone (NCBIN:121210, NCBIP:121213)
C; Superfamily: Pseudomonas putida regulatory protein catR
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C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: BB3451
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; BB
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                                                                     Length 483;
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100.0%; Pred. No. 12;
11ve 0; Mismatches
                                                               DB 2;
                                                               34.8%; Score 8; DB 2
llarity 100.0%; Pred. No. 1.5
Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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302 QAEGAEDE 309
                                 Query Match
Best Local Similarity
"...h.aa 8; Conserve
                                                                                                                                                                                             13 QAEGAEDE 20
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A; Note: F4D11.80
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A; Rolecule type: mRNA
A; Residues: 1-178 <-BED>
A; Molecule type: mRNA
A; Residues: 1-178 <-BED>
B; Descalz1, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto, J. Biol. Chem. 267, 2979-2985, 1992
A; Title: Expression. regulation, and tissue distribution of the Ch21 protein during c A; Reference number: A42581; MUID:92147639; PMID:1737754
A; Recession: A42581
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-95, L./, 97-178 <-DO2>
A; Residues: 1-95, L./, 97-178 <-DO2>
A; Residues: 1-95, L./, 97-178 <-DO2>
A; Reperimental source: tibia hypertrophic cartilage
A; Note: sequence extracted from NCB1 backbone (NCBIN:80796, NCBIP:80797)
B; Cancedda, F.D.; Dozin, B.; Rossi, F.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi, J. Biol. Chem. 265, 19960-19964, 1990
A; Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the A; Reference number: A36595; MUID:91035433; PMID:2229062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Resdues: 21-95, "L'9-178 <CAN>
A;Resdues: 21-95, "L'9-178 <CAN>
A;Cross-references: GB:M37611
B;Cancedda, F.D.; Asaro, D.; Molina, F.; Cancedda, R.; Caruso, C.; Camardella, L.; Ne
Blochem Biophys. Res. Commun. 168, 933-938, 1990
A;Title: The amino terminal sequence of the developmentally regulated CH21 protein sh
A;Reference number: A35491; MUID:90267487; PMID:2346493
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                                                                       NAlternate names: Ch21 protein
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1990 **sequence_revision 31-Dec-1990 **text_change 15-Nov-1996
C;Accession: A30230; A42581; A36595; A55491
R;Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A;Title: Rapid repression of quiescence-specific gene expression by epidermal growth
A;Reference number: A30230; MUID:89261749; PMID:2498647
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A,Molecule type: DNA
A,Residues: 1-180 <THO
A,STGSS-references: EMBL:AJ222725; PIDN:CAA10962.1
A;Experimental source: ATCC 15009
C,Genetics: plasmid pLH1
C;Superfamily: Lactobacillus helveticus plasmid pLH1 hypothetical protein ORF-180
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F. 1-21/Domain: signal sequence #status predicted <SIG>
F. 22-178/Product: quiescence-specific protein #status predicted <MAT>
F. 25-173/Domain: lipocalin homology <LIP>
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                                     quiescence-specific protein precursor - chicken
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Best Local Similarity 100.
Matches 6; Conservative
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A;Molecule type: protein
A;Residues: 21-48 <CA2>
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S; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Targa, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0401
A; Reference number: AB0401
A; Reterence number: Diagnosis preliminary
A; Molecule type: DNA
A; Residues: 1-142 < KUR>
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YPO3302 [imported] - Yersinia pestis (strain C092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0401
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C; Superfamily: major cold shock protein; cold shock domain homology
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                                                                               Length 69;
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100.0%; Pred. No. 57;
ive 0; Mismatches
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                                                                           DB 2;
                                                                       Query Match 26.1%; Score 6; DB 2, Best Local Similarity 100.0%; Pred. No. 32; Matches 6; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 6; Conservative
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A; Map position: 1
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C; Superfamily: 1
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|30 EGAEDE 135
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| 165 GQAEGA 170
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A; Molecule type: mRNA
A; Residues: 1-223 <SHI>
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C; Accession: D69070
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Mypothetical protein EC35625 [imported] - Escherichia coli (strain O157:H7, substrain RI Mypothetical protein EC35625 [imported] - Escherichia coli (strain O157:H7, substrain RI C; Species: Escherichia coli #1 acii #1 acii
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A;ExperImental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 24080 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
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K.; Apodaca,
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Specias: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 14 - Sep-2001 (Strain Davis, N.T.) Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Status: preliminary
A; Status: preliminary
A; Residues: 1-189 <STO>
                                                                                                             Gaps
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                                  DB 2;
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100.0%; Pred. No. 72;
:ive 0; Mismatches
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100.0%; Pred. No. 72;
iive 0; Mismatches
                              26.1%; Score 6; DB 3
100.0%; Pred. No. 69;
iive 0; Mismatches
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                          Query Match 26.1
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Figurith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubols, J.; Aldredge, T.; Glu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Glbson, R.; Jiwani, K.; S.; Chucch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69070
A;Accession: D69070
A;Accession: D69070
A;Molecule type: DNA
A;Molecule type: DNA
A;Retus: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: GB:AE000912; GB:AE000666; NID:92622632; PIDN:AAB85999.1; PID:9262
A;Experimental source: strain Delta H
A;Genetics:
C;Genetics:
A;Start codon: TTG
C;Start codon: TTG
C;Superfamily: amidotransferase hisH; trpG homology
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R;Shimizu, N.; Obta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H
J. Biol. Chem. 266, 12157-12161, 1991
A;Title: Expression of a novel immediate early gene during 12-0-tetradecanoylphorbol-
A;Reference number: A40866; MUID:91286224; PMID:2061303
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C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.1%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 75; Matches 6; Conservative 0; Mismatches
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us-09-853-253-6.oli.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 11, 2003, 17:30:37; Search time 4.42781 Seconds (without alignments) 244.278 Million cell updates/sec Run on:

1 ALAGWLRPEDGGQAEGAEDELEV US-09-853-253-6 23 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

23

0

Word size :

127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

127863

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Ogubu3 homo sapten		Q91127 streptomyce	-	_		P21760 gallus gall	E		P09491 drosophila		042431 limnocottus	Q9zk75 helicobacte	Q8p280 streptococc				P36944 bacillus su	Q8yi74 brucella me	Q10717 zea mays (m		Q09689 schizosacch	Q99t16 staphylococ		_	P78022 mycoplasma	_	Q9gmb8 bos taurus	P49591 homo sapien	P16098 hordeum vul	Q12899 homo sapien	kix3	074261 candida alb
	ID	GHRL HUMAN	GHRL_BOVIN	MPR2_STRCO	MPRR_STRLI	V120_EBV	GHRL_CANFA	EFAB_CHICK	HIS5_METTH	COLI_PIG	TPM2_DROME	PCD1_HUMAN	OPSD_LIMPA	PARB_HELPJ	MTSA_STRP8	MTSA_STRPY	MRAW_XYLFA	YF56_HAEIN	RBSR_BACSU	MRAW_BRUME	CYS2_MAIZE	PURK_BACSU	IF5_SCHPO	TIG_STAAM	CUS1_YEAST	RPSD_MYCGE	RPSD_MYCPN	SYS_MOUSE	SYS_BOVIN	SYS_HUMAN	AMYB_HORVU	Z173_HUMAN	CH60_BUCTC	HS60_CANAL
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P19882 saccharomyc P50142 ajellomyces	Q92154 coturnix co P26242 rhodobacter P51693 homo sapien	P35492 mus musculu O14978 homo sapien	Q9yfq8 aeropyrum p Q9z512 streptomyce	O54951 mus musculu O70141 rattus norv	P25516 escherichia
HS60_YEAST HS60_AJECA	SMP_COTJA DXS_RHOCA APP1_HUMAN	HUTH_MOUSE 2263_HUMAN	HELS_AERPE UVRC_STRCO	SM6B_MOUSE SM6B_RAT	ACO1_ECOLI
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ALIGNMENTS

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Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
GHRL_HUMAN STANDARD; PRT; 117 AA.
09UBU3; 09H3R3;
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
6hrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomasetto C., "Arram S.M., Rio M.-C.; "Identification of a novel gastric protein m46."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
Welntajch M.P., Ten I.S., Gertner J.M., Leibel R.L.;
Genomic organization of the human Ghreiln gene.";
J. Endocrinol. Genet. 1:231-233(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GHRELIN (BY SIMILARITY).

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K -> E (IN REF. 2).

F SSSSSOACSFASSB6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                           GHRL_BOVIN STANDARD; PRT; 116 AA.
09BDJ6; 09GKY6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
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                                                            Length 117;
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Pred. No. 0.0013;
0; Mismatches 0; Indels
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
   117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
                                                         100.0%; Score 23; DB 1; I 100.0%; Pred. No. 5.4e-17;
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InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
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                                                                                                                  Conservative
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51
26
34
116 AA;
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Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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Best Local Simi
Matches 10;
   SEQUENCE
                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/GhrelinID327.html".

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO: GO:0005615; C:extracellular space; TAS.
GO: GO:0005625; C:soluble fraction; TAS.
GO: GO:0005131; F:growth hormone receptor ligand activity; TAS.
GO: GO:0007267; P:cell-cell signaling; TAS.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro: IPR006737; motilin_assoc.
InterPro: IPR006738; motilin_assoc.
InterPro: IPR006741; Preproghtelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trends Endocrinol. Metab. 12:116-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite retimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-21203998; PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Pram; PF01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                              Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms-2;
Name-1; Synonyms-Ghrelin;
IsoId-Q9UBU3-1; Sequence-Displayed;
Name-2; Synonyms-Gal-Gin14-ghrelin;
IsoId-Q9UBU3-2; Sequence-VSP_003245;
PTM: O-n-octanoylation is essential for activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform 2).
/FTId=VSP_003245.
L -> M (IN REF. 5).
                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth regulation.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                     TISSUE-Stomach;
MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB029434; BAA89371.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone secretagogue receptor.
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                                                         and mouse cDNA sequences.
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EMBL; AF296558; AAG10
EMBL; BC025791; AAH25
PIR; AS9316; A59316.
MIM; 605353;
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                                                                                                                                             SEQUENCE OF 24-33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 111:125-130(1992).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE
                                                                                                                                                                                                                                                                                                                Streptomyces lividans 66: a novel neutral protease activity in adjacent divergent putative regulatory gene."; Can. J. Microbiol. 38:912-920(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O., McGinley M.O., Rohde M.F., Katzowitz J.L., Zukowski M.M.; "Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMALL NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                      Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T.;
"Cloning of genetic loci involved in endoprotease activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M81703; AALE6804.1; ALL.
EMBL; M89476; AAA26804.1; ALL.
EMBL; M89476; AAA26804.1; ALL.
InterPro; IPR005119; LysR_subst.
3R Drem; PF00126; HTH_1; LysR_subst.
3R Pfam; PF00126; HTH_1; LysR_subst.
3R Pfam; PF03466; LysR_substrate; 1.

DR PR0STITE; PS00044; HTH_LYSR_FAMILY; 1.

TAGGOSTE; PS00044; HTH_LYSR_FAMILY; 1.

TAGGO
                                                      Streptomyces lividans.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.4%; Score 7; DB 1;
100.0%; Pred. No. 4.2;
iive, 0; Mismatches
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21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Small neutral protease regulatory protein
                                                                                                                                                                                                                                                STRAIN=66 / 1326;
MEDLINE=93099553; Pubmed=1464066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92192468; PubMed-1547948;
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Matches 7; Conservative,
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                                                                                                                                                         NCBI_TaxID=1916;
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                                MPRR OR SNPR
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ID V120_EBV
AC P03189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Gronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Sebbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Senders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2).";
Nature 417:141-147(2002).
-1- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR THE SMALL NEUTRAL PROTEASE.
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Pfam: PF03466; LysR_substrate; 1.
PRINTS: PR00039: HTHLISR.
PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
DNA-binding: Procease: Transcription regulation; Complete proteome.
DNA-binding: PC0 39 H-T-H MOTIF (POTENTIAL).
SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 7; DB 1; Length 328; 100.0%; Pred. No. 4; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5mall neutral protease regulatory protein.
STREPTOMYCES COELICOLOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32, Created)
32, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                328 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL939131; CAB76352.1; -.
InterPro; IPR000847; HTH_LysR.
InterPro; IPR005119; LysR_subst.
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Matches 7; Conservative
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                            OAEGAEDELE 72
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(Rel.
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01-NOV-1995 (
01-NOV-1995 (
28-FEB-2003 (
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Q9L127;
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MPRR_STRLI
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Gaps

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0; Indels

PRT; 1239 AA.

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or send an email to license@isb-sib.ch).
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PROPEP
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                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@laborath.ch).
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             Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Haffull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G., "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-!PUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducting the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=Q9BEF8-2; Sequence=VSP_003244;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                    Nature 310:207-211(1984).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
EHV-1 23, EBV BOLF1, V2V 21, HVS-1 63, AND HCMV UL47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE-Gastric fundus;
Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
"Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHRL_CANFA STANDARD; PRT; 117 AA.
09BEF8; 09BEF7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                       30.4%; Score 7; DB 1; Length 1239; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                            PIR; A43041; QOBE10.
Capsid assembly.
SEQUENCE 1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    releasing peptide) (Motilin-related peptide).
GHRL OR MTLRP.
                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ...
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IsoId=Q9BEF8-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
 MEDLINE-84270667; Pubmed-6087149;
                                                                                                                                                                                                                                              EMBL; V01555; CAA24841.1; -.
                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 7; Conservative
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696 AEGAEDE 702
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Matches
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SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-91035433; PubMed-2229062;
Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
Negri A., Ronchi S.,
"The Ch21 protein, developmentally regulated in chick embryo, belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89261749; PubMed-2498647;
Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
"Rapid repression of quiescence-specific gene expression by epidermal growth factor, insulin, and pp60v src.";
Mol. Cell. Biol. 9:1371-1375(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giannonl P., Dozin B., Zambotti A., Neri M., Cancedda R.; "Differentiation-dependent activation of the extracellular fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
Hayashi K., Quarto R., Cancedda R.;
Hayashi K., Quarto R., Cancedda R.;
"Expression, regulation, and tissue distribution of the Ch21 protein during chicken embryogenesis.";
J. Biol. Chem. 267:2979-2985(1992).
                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                      basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding protein (EXPABP) gene in chicken embryo chondrocytes.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P21760; P21928; Q9PWN9; 01-MAY-1991 (Rel. 18, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Extracellular fatty acid binding protein precursor (Ex-FABP) (Quiescence-specific protein) (P20K) (Ch21 protein).
                                                                                                                                                                                                                                                                                                                                                   GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIN-CTANOATE (BY SIMILARITY).
MISSING (In 1806form 2).
//FTId=VSP_003344.
A; 3E57FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.1%; Score 6; DB 1;
100.0%; Pred. No. 18;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AA
                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                              EMBL, A4292950, CACASTOOT, T. S. C. InterPro; IPR006737; Motilin_assoc. InterPro; IPR006738; Motilin_ghrelin. InterPro; IPR005441; Preproghrelin. Pfan; PF04643; Motilin_assoc; 1. Pfan; PF04644; Motilin_assoc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                        PRINTS; PRO1624; GHRELIN.
PRODOM; D333162; Preproghrelin; 1.
HORMONG; Cleavage on pair of basic
Alternative splicing
EMBL; AJ298295; CAC29155.1; -. EMBL; AJ298296; CAC29156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA; 13007 MW;
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Gallus gallus (Chicken).
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 AEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEDELE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
                                                                                                                    MEDLINE-90267487; PubMed-2346493; Cancedda R., Caruso C., Canardella L., Negrl A., Ronchl S.; Camardella L., Negrl A., Ronchl S.; The amino terminal sequence of the developmentally regulated Ch21 protein shows homology with amino terminal sequences of low molecular weight proteins binding hydrophobic molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Descalzi Cancedda F., Dozin B., Zerega B., Cermelli S., Cancedda R.;
"Ex-FABP: a fatty acid binding lipocalin developmentally regulated in chicken endochondral bone formation and myogenesis.";
Blochim. Blophys. Acta 1482:127-115(2000).

-I- FUNCTION: Preferentially binds long-chain unsaturated fatty acids such as linoleic acid, oleic acid, arachidonic acid. Also binds with a lower affinity long chain saturated fatty acids such as steraic acid. May act as survival protein by playing a role in maintaining cell viability.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 103-178 FROM N.A.
STRAIR-white legitorn; TISSUB-Bone marrow;
MEDLINE-92195590; PubMed-1549365;
Nakano T., Graf T.;
"Identification of genes differentially expressed in two types v-myb-transformed avian myelomonocytic cells.";
oncogene 7:527-534(1992).
the superfamily of 11pophilic molecule carrier proteins."; Biol. Chem. 265:19060-19064(1990).

    MISCELLANEOUS: Developmentaily regulated in chick embryo.
    SIMILARITY: Belongs to the lipocalin family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancedda F.D., Malpell M., Gentili C., Dl Marzo V., Bet P., Carlevaro M., Cermelli S., Cancedda R.; The developmentally regulated avian Ch21 lipocalin is an extracellular fatty acid-binding protein."; J. Biol. Chem. 271:20169-11996).
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L -> S (IN REF. 2).

R -> S (IN REF. 2 AND 4).

F -> S (IN REF. 2 AND 4).
                                                                                                                                                                                                                                                                                                  Blochem. Blophys. Res. Commun. 168:933-938(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- PTM: Does not seem to be glycosylated.
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BY SIMIL
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InterPro; IPR000566; Lipocln_cytFABP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20513977; PubMed=11058755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96355330; PubMed-8702740;
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PROSITE, PS00213, LIPOCALIN; 1.
Lipocalin; Transport; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00061; lipocalin; 1.
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., RA MILLINE-SBUJJOINE, TUDMOGED T., Bashizadeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Bashizadeh R., Blakely D., Cook R., Gilbert K., Bashizadeh R., Wang Y., Lumm W., Pothler B., Olu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum RT deltaH: functional analysis and comparative genomics."; Collish J. 1735-7155 (1997).

J. Bacteriol. 179:7135-7155 (1997).

J. Bacteriol. 179:7135-7155 (1997).

J. Bacteriol. 179:7135-7155 (1997).

J. FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine ammonian necessary to IGP, AICAR and glutamate. The hisH subunit provides the glutamine aminoince and glutamate. The hisH subunit provides the glutamine conversion of IGP and AICAR (By similarity).

J. CATALYTIC ACTIVITY: 5-{{5-phospho-1-deoxyribulos-1-carboxamide + L-glutamine - imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamine - imidazole-glycerol phosphate + 1-subunit atterodimer of hish attellar step:

J. SUBUNIT: Heterodimer of hish and hish Responsible to the Sultamine amidotransferase domain.

J. SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last anomatical update)
28-FEB-2003 (Rel. 41, Last anomatical update)
Imidazole glycerol phosphate synthase subunit hish (EC 2.4.2.-) (IGP synthase glutramine amidotransferase subunit) (IGP synthase subunit hish) (IMGP synthase subunit hish)
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; _IPR000991; GATase_1.
Pfam; PF00117; GATase; 1.
PROSITE; PS00442; GATASE TYPE_I; 1.
Histidine blosynthesis; Transferase; Glutamine amidotransferase;
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                    Length 178;
                                                                                                                            0; Indels
F -> S (IN REF. 1).
L -> V (IN REF. 1).
ODDBDC33C1A0C6B8 CRC64;
                                                                                    Score 6; DB 1;
                                                                                                                                                                                                                                                                                                                       198 AA
                                                                                                 100.0%; Pred ...
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                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
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InterPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
                                          20201 MW;
                                                                                  26.1%;
                                                                                                                              Conservative
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62
96
178 AA;
                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                       18 EDELEV 23
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ACT_SITE 77
ACT_SITE 177
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O27568;
                                                                                      Query Match
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MEDLINE-74306590; PubMed-4369114;
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                                                                                                                                                          COLI_PIG STANDARD; PRT; 267 AA.
P01192; 095246;
21-JUL-1986 (Rel. 01, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-1001 (Rel. 40, Last annotation (Adrenocorticotropin damma (Gamma-MSH); Melanotropin alpha (Alpha-MSH);
17-DOLICOPIN gamma (Gamma-LPH); Melanotropin beta (Beta-Beta-endorphin; Met-enkephalin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of porcine and rat pro-opiomelanocortin mRNA. One porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-55046635; Pubmed=7958386;
Gen K., Hirai T., Kato T., Kato Y.;
Hresence of the same transcript of pro-opiomelanocortin (POMC) genes
in the porcine anterior and intermediate pituitary lobes.";
Mol. Cell. Endocrinol. 103:101-108(1994).
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolleau G., Barbeau C., Jeannotte L., Chretien M., Drouin J.; "Complete Structure of the porcine pro-opiomelanocortin mRNA derived from the nucleotide sequence of cloned cDNA."; Nucleic Acids Res. 11:8063-8071(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 136-174.
Shepherd R.G., Willson S.D., Howard K.S., Bell P.H., Davies D.S., Davies S.B., Eigner E.A., Shakespeare N.E.;
Studies with corticotropin. III. Determination of the structure of beta-corticotropin and its active degradation products.";
J. Am. Chem. Soc. 78:5067-5076(1956).
                                                                                                                                                                                                                                                                                                               Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86131687; PubMed-3753882;
Gossard F.J., Chang A.C.Y., Cohen S.N.;
"Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
Biochim. Biophys. Acta 866:68-74(1986).
                                 Length 198;
                                                         Indels
BY SIMILARITY.
E8EFA43EC9163AEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-72114902; PubMed-4334191;
Riniker B., Sleber P., Rittel W., Zuber H.;
Revised amino-acid sequences for porcine and human
adrenocotticotrophic hormone ";
Nature New Biol. 235:114-115(1972).
                                 Score 6; DB 1;
Pred. No. 28;
                         26.1%; Scor.
100.0%; Pred. No. 2.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and two rat forms.";
J. Biol. Chem. 259:7421-7425(1984).
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MEDLINE-84239667; PubMed-6547437;
Oates E., Herbert E.;
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MEDLINE-84069823; Pubmed-6196724;
          21348 MW;
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                                                        6; Conservative
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBL_TaxID=9823;
179 1
198 AA;
                                                                                           130 EGAEDE 135
                                Query Match
Best Local Similarity
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ACT_SITE
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MEDLINE-76100762; Pubmed-1207728;
Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
Morris H.R.;
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MEDLINE-77084500; PubMed=1007884;
Graf L., Barat E., Patthy A.;
"Isolation of a COOH-terminal beta-lipotropin fragment (residues 61-91) with morphine-like analgesic activity from porcine pituitary glands.";
                                                                                                                         SEQUENCE OF 136-174.

MEDLINE-91071194; PubMed-2174774;
Volgt K., Stegmaler W., McGregor G.P., Roesch H., Seliger H.;
Volgt K., Stegmaler W., McGregor G.P., Roesch H., Seliger H.;
"Isolation and full structural characterisation of six
adrenocorticotropin-like peptides from porcine pituitary gland.
Identification of three novel fragments of adrenocorticotropin and two forms of a novel adrenocorticotropin and in Blochem. 194:225-236(1990).
'Re-examination of the sequence of the C-terminal tryptic fragment from porcine adrenocorticotropic hormone."; Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             porcine beta-lipotropic hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pankov Y.A., Yudaev N.A.;
"Complete amino acid sequence in the molecule of porcine beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: BETA-ENDORPHIN AND MET-ENKEPHALIN ARE ENDOGENOUS
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Harris J.I., Roos P.;
"Amino-acid sequence of a melanophore-stimulating peptide.";
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"The structure of the beta-melanocyte-stimulating hormone.";
J. Am. Chem. Soc. 79:620-625(1957).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQÜENCE OF 177-267.
MEDLINE-7111231; PubMed-5543613;
Mard L., Barat E., Cseh G., Sajgo M.;
"Amino acid sequence of porcine beta-lipotropic hormone.";
Biochim. Biophys. Acta 229:276-278(1971).
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"Complete amino acid sequence of porcine beta-lipotropic (beta-LPH).";
(In) Weienhofer J. (eds.);
Chenistry and biology of peptides, pp.609-611, Ann Arbor Ann Arbor (1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 211.
MEDLINE=73048217; PubMed=4673865;
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melanogaster.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of Swiss are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD THE DIFFERENT ACTIVE PEPTIDES.
-!- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELANOTROPIN ALPHA.
CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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AMIDATION (G-149 PROVIDE AMIDE GROUP).
N-LINKED (GLCNAC. . ) (POTENTIAL).
R -> T.
G -> S (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                            Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D TYPAZ DROWE STANDARD; PRT; 284 AA.

C P09491; P09490; Q24408; Q24427; Q24428; Q8SZ65; Q9VF95;

T OL HAR-1989 (Rel. 10, Created)

OL HAR-1989 (Rel. 10, Last sequence update)

T 15-SEP-2003 (Rel. 42, Last annotation update)

T Tropomyosin 2 (Tropomyosin I).

E Tropomyosin 2 (Tropomyosin I).

N TWZ OR TWI OR CG4843.

S Drosophila melanogaster (Fruit fly).

E Ukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Ephydroidea; Drosophilade; Drosophilade; Drosophila.
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G -> S (IN REF. 3 AND 4).

T -> A (IN REF. 3 AND 4).

G -> E (IN REF. 3 AND 4).

A -> S (IN REF. 4).

A -> S (IN REF. 4).

W; A6DB487A5032B648 CRC64;
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LIPOTROPIN GAMMA.
MELANOTROPIN BETA.
BETA-ENDORPHIN.
MET-ENKEPHALIN.
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9
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Pred. No
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MEDLINE-84205681; PubMed-6202423;
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ilarity 100.0%; Pr
Conservative 0;
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PRINTS; PR00383; MELANOCORTIN
                                                                                                                                                                                                                                                                   X00135, CAA24968.1; -. S73519, AAB32312.1; -. K01879; AAA31104.1; -.
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| GAEDEL 166
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267 AA;
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Best Local Similarity
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10 TPM2_DROME
DT 01-MAR
DT 01-MAR
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DE TROPOMY
GN TROPOMY
CC ENKRIY
CO NEOPTE
CO NEOPT
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                                                                                      (PDCD1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLFNEKEKYKALCDDLDQTFAELTGY -> ELGINKDRYKS LADEMDSTFAELAGY (in isoform Embryonic). /FTId=VSP_006616.
                                                                                       Event=Alternative splicing; Named isoforms=2;
Name=Thoracic; Synonyms=127, t;
Isold=P09491-1; Squence=Displayed;
Name=Embryonic; Synonyms=129, A, B, e;
Isold=P09491-2; Squence=VSP_006616;
DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE STHILARTY: BELONGS TO THE TROPOMYOSIN FAMILY.
CAUTION: Ref. 6 sequence differs from that shown due to erroneous gene model prediction.
                             MEDLINE-85215579; PubMed-4000944;
Boardman M., Basi G.S., Storti R.V.;
"Multiple polyadenylation sites in a Drosophila tropomyosin gene are used to generate functional mRNAs.";
Nuclaic Acids Res. 13:176(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCD1_HUMAN STANDARD; PRT; 288 AA.
0105116; 000517;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Programmed cell death protein 1 precursor (Protein PD-1) (hPD-1).
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PROSITE; PS00326; TROPOMYOSIN; 1.
Muscle protein; Colled coil; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 284;
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Q -> L (IN REF. 1).

I -> T (IN REF. 1).

I -> T (IN REF. 1).

R -> D (IN REF. 1).
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                    SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Score 6; DB 1
100.0%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X02220; CAA26142.1; ALT_SEQ.
PIR; A25624; A25624.
PIR; B25624; B25624.
                                                                                                                                                                                                                                                                                         EMBL; K02622; AAA28970.1; -.
EMBL; K02623; AAA28971.1; -.
EEMBL; K03622; AAA28971.1; JOINED.
EMBL; K03377; AAA28973.1; -.
EMBL; K03277; AAA28974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              Flybase, FBgn0004117; Tm2.
InterPro; IPR000533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                11 11 M
88 88 Q
95 95 1
255 255 I
284 AA; 32981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      fam; PF00261; Tropomyosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 EDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
9
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CONFLICT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-9473511; PubMed-9332365;
Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
"The human PD-1 gene: complete cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
Gene 197:177-187(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finger L.R., Pu J., Wasserman R., Vibhakar R., Loule E., Hardy R.R., Burrows P.D., Billips L.D.;

Gene 203.253-534(1997).

-i - FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                       MEDIINE-95154844; Pubmed-7851902;
Shinohara T., Taniwaki M., Ishida Y., Kawalch M., Honjo T.;
"Structure and chromosomal localization of the human PD-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGRAMMED CELL DEATH PROTEIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: 00:0004071; F:signal transducer activity; TAS. GO: 00:0006915; P:apoptosis; TAS. GO: 00:0007275; P:development; TAS. GO: GO:0000595; P:humoral immune response; TAS. InterPro; IPR007110; Ig-11ke.
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P -> S (IN REF. 1).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31707 MW;
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                                                                                                                                                                                                                                                     Genomics 23:704-706(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
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192
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116
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Matches 6; Conserv
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(POTENTIAL).

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CYTOPLASMIC (
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; H71852; H71852.
InterPro; IPR004437; ParB_part.
InterPro; IPR003115; ParBc.
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100.0%;
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Best Local Similarity 100....
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281 >2
81 267
171 289
289 AA;
                                                                                                                                                                                                                    143 LAGWLR 148
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Best Local Similarity
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                                                                                                                                                                                               2 LAGWLR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PARB OR JHP1066
                                                                                                                                                                                                                                                                                                                        PARB_HELPJ
Q92K75;
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16-OCT-2001
 DOMAIN
DISULFID
                                                  CARBOHYD
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SEQUENCE
                                     BINDING
                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Scorpaeniformes, Cottoidei, Abyssocottidae, Limnocottus.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98086781; Pubmed-9417898;
Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR00176; Opsin.
InterPro; IPR00176; Opsin.
InterPro; IPR00101; Ttm_1; 1.
PRINTS; PR000237; GPCRRHODOPSN.
PROSITE; PS000237; G_PROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS00238; OPPINI. RECEP_F1_2; 1.
                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Rhodopsin (Fragment).
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                                                                                                                         STANDARD;
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44
69
84
104
147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPSIN SUBFAMILY.
                  111111
277 LRPEDG 282
6 LRPEDG 11
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=61634;
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                                                                                   RESULT 12
OPSD_LIMPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99120557; PubMed-9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter priori 199 (Campylobacter pylori 199).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence comparison of two unrelated isolates of the human
RETINAL CHROMOPHORE (BY SIMILARITY).
                                N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                  Length 289
                                                    289
32715 MW; 160D08E17E5E1280 CRC64;
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TIGREMS; TIGRO180; parB_part; 1.
Chromosome partition; DNA-binding; Complete proteome.
SEQUENCE 290 AA; 33405 MW; 6709BA0547A55A4F CRC64;
                                                                                                                                                  DB 1;
5. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable chromosome partitioning protein parB
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                                                                                                                                               26.1%; Score 6; DB 1
100.0%; Pred. No. 39;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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InterPro
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STRAINWAGASB232 / Serotype M18;

MEDLINE-21927593; PubMed-11917108;

MEDLINE-21927593; PubMed-11917108;

Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

Rapur V., Daly J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype M18

"Genome sequence and comparative microarray analysis of serotype M18

"Genome sequence and comparative microarray analysis of serotype M18

"Group A Streptococcus strains associated with acute rheumatic fever

outbreaks."

"In Proc. Natl. Acad. Scl. U.S.A. 99:4668-4673(2002).

"In Proc. Natl. Actached to the membrane by a lipid anchor.

"In SUBCELLUAR LOCATION: Attached to the membrane by a lipid anchor.

"In Proc. Natl. Actached to the membrane by a lipid anchor.

"In SUBCELLUAR LOCATION: Attached (Lia) subfamily anchor.
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Metal ABC transporter substrate-binding lipoprotein precursor.
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09A157; 09RN17; 09RNJ0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Metal ABC transporter substrate-binding lipoprotein precursor.
MTSA OR SPY0453 OR SPYM3_0318 OR SPS1539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006127; SBP_bac_9.
InterPro; IPR006127; SBP_bac_9.
Pfam; PF01297; SBP_bac_9; 1.
PRINTS; PR00690; ADHESNFAMILY
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Transport; Zinc transport; Iron transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSPORTER SUBSTRATE
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N-ACYL DIGLYCERIDE (PROBABLE).
40F613659AAD1768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
                                                                                                        Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes, and
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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100.0%; Pred. No....
0; Mismatches
           310 AA.
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          PRT;
                                       (Rel. 41, Created)
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Best Local Similarity 100.
Matches 6; Conservative
           STANDARD;
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SIGNAL 1
                                                                                           MTSA OR SPYM18_0494.
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310 AA;
                                                                                                                                                 NCBI_TaxID=186103;
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                                                                                                                                     Streptococcus
                                     28-FEB-2003
          MTSA_STRP8
Q8P280;
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MTSA_STRPY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SERJO / ATCC 700294 / Serotype M1;
MEDLINE=21192684; Pubmed=11296206;
MEDLINE=21192684; Pubmed=11296206;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roee B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Scl. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-2003232; PubMed-10564500;
Janulczyk R., Pallon J., Bjoerck L.;
Janulczyk R., Pallon J., Bjoerck L.;
"Identification and characterization of a Streptococcus pyogenes ABC
transporter with multiple specificity for metal cations.";
Mol. Microbiol. 34:596-606(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133008; Pubmed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlibevert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION. STRAIN-SF370 / ATCC 700294 / Serotype M1, and AP1 / Serotype M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
METAL ABC TRANSPORTER SUBSTRATE-BINDING LIPOPROTEIN,
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PRINTS; PR00690; ADHESNFAMILY.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Transport; Zinc transport; Iron transport; Copper; Membrane; Lipoprotein; Signal; Complete protecme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACYL DIGLYCERIDE (PROBABLE).
V -> A (IN STRAIN AP1).
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EMBL, AE006505; AAK33468.1; -.
EMBL; AE014143; AAM78925.1; ALT_INIT.
EMBL; AP005145; BAC64634.1; ALT_INIT.
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Streptococcus.
NCBI_TaxID=1314, 198466;
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VARIANT
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FT CONFLICT 26 26 T -> A (IN REF. 1).
FT CONFLICT 30 30 K -> E (IN REF. 1).
FT CONFLICT 49 40 A -> G (IN REF. 1).
FT CONFLICT 49 50 A -> G (IN REF. 1).
SQ SEQUENCE 310 AA; 34358 MW; B0F829EFIC72CADC CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 EDGGQA 14
Db 94 EDGGQA 99

Search completed: September 11, 2003, 17:52:41
Job time: 4.42781 secs
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                                                     Q65548 bovine herp
O43180 homo sapien
Q8Jfy6 litoria cae
Q8n8h9 homo sapien
P93359 nicotiana t
                            226847 trypanosoma
Q8g7n5 bifidobacte
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              087801 pseudomonas
Q26847 trypanosoma
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Blood;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025791; AAH25791.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
SEQUENCE 117 AA; 12929 WW; 25B0572EBECB7610 CRC64;
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Q8N8H9
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Q25619
Q8MZJ8
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Q25622
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O43180
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Q8WT56
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QBCH53;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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 Query Match
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Q932v7 arabidopsis
Q817e4 arabidopsis
Q81063 streptomyce
Q8vp52 streptomyce
Q8vp52 streptomyce
Q8vy49 ralstonia s
Q9413f5 pseudomonas
Q9540 drosophila
Q966v1 drosophila
Q965v1 drosophila
Q952v1 gyrobaculum
P91785 onchocerca
Q8pbn4 xanthomonas
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269.586 Million cell updates/sec
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              GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                   OM protein - protein search, using sw model
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PRELIMINARY;
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01-OCT-2002
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
A Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamanura Y., Yu G.,
Yu S., Bowser L., Carninci P., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
A Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
A Nguyen M., Palm C.J., Sakurai T., Satcu M., Seki M., Shinn P.,
A Theologis A.;
Full Length CDNA of gene Ar4932720 (GI:7270219).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY05637; AAL07086.1;
RinterPro; IPR006630; Lupus_La.
RinterPro; IPR006630; Lupus_La_dom.
RinterPro; IPR006630; Lupus_La_dom.
RinterPro; IPR006630; Lupus_La_dom.
RinterPro; IPR006630; RNA_rec_mot.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                      Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                                                                                                                                            "NUCLE OF THE WONGOLIAN GENDIL PREPONDENT MENNA.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF442491; AAO06965.1; -.
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                      Ghrelin preproprotein.
Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                    47.8%; Score 11; DB 11; Length 11
100.0%; Pred. No. 0.00062;
ive 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative RNA-binding protein LAH1.
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50102; RRM;
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287 QAEGAEDE 294
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                       Meriones.
NCBI_TaxID-10047;
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                                                                                                                                                                                                                                             Ishii H.;
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0932V7
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A Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
A Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
A Chung M. K., Hayashizaki Y., Ishlada J., Kamiya A., Kawai J.,
A Kim C., Lin J., Liu S.X., Barusaka M., Pham P.K., Sakano H.,
A Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
B Cabmitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
C Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
B CHEAPTO, IPRO0154 F. Lupus_La.
B CHEAPTO, IPRO06501, Lupus_La.
B CHEAPTO, IPRO06501, Lupus_La.
B CHEAPTO, IPRO06501, Lupus_La.
B CHEAPTO, IPRO0151, La.
B CHEA
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Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Torcumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Tu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 54.1 kDa protein.
F4D11.80 OR AT4G32720.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Benes V., Rechmann S., Borkova D., Ansorge W., Hoheisel J.,
Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                  Last sequence update)
Last annotation update)
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100.0%; Pred. No. 2.8;
iive 0; Mismatches
      Created)
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(TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 23,
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                                                                                                                                                                                   Hypothetical protein. AT4G32720.
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287 QAEGAEDE 294
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Best Local Similarity
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SEQUENCE FROM N.A. STRAIN-ATCC 12228;
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            Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3(2)."};
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0
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Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL022537; CAA188589.1; ...
InterPro; IPR002344; Lupus_La.
InterPro; IPR00530; Lupus_La.
InterPro; IPR005630; Lupus_La.
InterPro; IPR00564; RNA_rec_mot.
Pfam; PP00076; rrm; I.
                                                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 417:141-147(2002).
EMBL; AL939114; CAB87228-1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) .
01-UMAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein SC02791.
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STRAIN-A3(2) / M145;
MEDLINE-21996410; Pubmed-12000953;
                                                                                                                                                                                                                                                                                                                     PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
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Matches 8; Conservative
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302 QAEGAEDE 309
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                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Q9L063
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016748; AAO04949.1; -
                                                                                                                                                                                                                                                                                  STRAIN=C5;
Besarti C.L., Strohl W.R.;
"Cheracterization of the Streptomyces sp. strain C5 snp locus and development of an snp-derived expression vector family.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                   LysR-like transcriptional activator SnpR.
Streptcmyces sp. C5.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=45212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AYOTZOAT,
InterPro; IPR000847; HTH LysR.
InterPro; IPR001847; HTH LysR.
InterPro; IPR05119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSTE; PS00044; HTH_LYSR.
DNA-binding; Transcription; Transcription regulation.
SEQUENCE 313 AA; 34258 MW; C907C8AF5LC3FA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 AA; 48732 MW; FF2490AD097F437D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8CNY4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trigger factor.
08VP52 PRELIMINARY; PRT; 313 AA. 08VP52: 11 MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2002 (TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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5. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.4%; Score 7; DB 1 (100.0%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 7; E
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Matches 7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 ALAGWLR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 DGGQAEG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 DGGQAEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLR 7
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Q8XY49
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910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;

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Complete proteome. SEQUENCE 910 AA;
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                                                                                                                                                  RESULT 11
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STRAINATCC 15692 / PAO1;
MFDLINE-20437337; Pubmed-10984043;
STRAINATCC 15692 / PAO1;
STORY C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulisen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                     Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Frenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                           DB 16; Length 887;
                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                 887 AA; 94105 MW; 9A8840E5362E740E CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Probable phage-related tail transmembrane protein.
RSC1914 OR RSO3483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 AA.
                                                                                                                                                                                                                                                                                                                                        59;
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100.0%; Pred. No. 59;
iive 0; Mismatches
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ProDom; PD000511; Aconitase_N; 1.
TIGRFAMs; TIGR01341; aconitase_1; 1.
                                                                                                                                               STRAIN-GMI1000;
MEDLINE-21681879; Pubmed-11823852;
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InterPro; IPR006249; Aconitase_1.
InterPro; IPR0010579; Aconitase_C.
InterPro; IPR001100; Aconitase_N.
Pfam; PP00330; aconitase; 1.
Pfam; PF00694; Aconitase_C: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
                                                                                                                                                                                                                                                                           EMBL; AL646067; CAD15616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004584; AAG04951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                         Query Match 30.4
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                  290 GOAEGAE 296
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                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Complete proteome
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.-H.C., Blazej R.G., Changhem M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendall B.C., Changhem M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendall J., Bayaraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendall J., Bayaraktaroglu L., Beasley E.M.,
RA Ballew R.M., Baut A., Butler H.J., Addrews-Pfannkoch C., Bolshakov S.,
RA Burtis R.C., Busam D.A., Buller H., Boutler L., Bolshakov S.,
RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Gavenport L.B., Davies P.,
RA Clodek R., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
Albin D., Houston K.A., Howland T.J., Hernandez J.R., Harris M.,
Alalli M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Jalli M., Kalush F., Karpen G.H., Re Z., Kennison D.A.,
Merkulov G., Milshina N.V., Li J.J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., Morfnosh T.C., Morendom D.M., Nesheel F., Smith T.,
Ralzzolo M., Pittum G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Rabiert K., Mong M., Murphy B., Murphy L., Wassenbach J.,
Rabiert K., Sanden D.A., Welsenbach J.,
Rabiert E., Spradling A.C., Stapleton M., Strong G., Zhoo O., Zhang Y.,
Wang Z.-Y., Wassarman D.A., Wellschele F., Wang S., Yao Q.A.,
Rabiert K., Zhong T.W., Zhong W., Zhou S., Zhu S., Zhoo O., Zhang Y.,
Rabeng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu S., Zhang Y.,
Rabeng R. H., Re G., Zhong W., Zhou S., Zhu S., Zhu S., Shith H.O.,
Rabeng R. H., Re G., Sunger P., Sanith H.O.,
Rabeng R. H., Re G., Shong W., Zhong G., Zhao O., Zhang L.,
Rabeng 
                                                                                                                            Gaps
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Elens C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                             DB 16;
                                     30.4%; Score 7; DB 10 100.0%; Pred. No. 60; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG18408 protein.
REXIN OR CG3451 OR CG18408 OR CG18409.
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Query Match
Best Local Similarity luv...
7; Conservative
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                                                                                                                                                                                                                                                                                     65 ALAGWLR 71
                                                                                                                                                                                                       1 ALAGWLR 7
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NCBI_TaxID=7227;
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us-09-853-253-6.oli.rspt

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-! - SIMILARITY: CONTAINS 3 SH3 DOMAINS
                       EMBL; AB05478; BAB62017.1; FlyBase; FBgn0033504; rexin.
InterPro: PFR002055; P_rich_extensn.
InterPro: IPR002055; P_rich_extensn.
Pfam; PF00018; SH3; 3.
                                                                                                                                                Pridm, F. PROL217; PRICHEXTENSN. ProDom; PD000066; SH3; 3. SMART; SM0326; SH3; 3.
                                                                                                                                                                                                        SMART; SM00326; SH3; 3. PROSITE; PS50002; SH3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=155892;
                                                                                                                                                                                                                                                         SH3 domain.
                                                                                                                                                                                                                                                                                   SEQUENCE
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Q9A542;
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Q8ZZR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annottation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferifera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., MOW M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittana G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melangaster genome.", Sequencing of Drosophila melangaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 7; DB 5; Length 2376; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2376 AA; 267666 MW; ASF2D0589BBB695C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003830; AAF58816.2; -.
FlyBase; FBgn0033504; rexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rexin L1.
REXIN OR RXN OR CG3451 OR CG18408 OR CG18409.
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PRINTS; PR00452; SH3DOMAIN.
PRODOM; PR000066; SH3; 3.
SMART; SM00326; SH3; 3.
PROSITE; PS50002; SH3; 3.
SEQUENCE 2376 AA; 267666 M
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Best Local Similarity 100.
Matches 7; Conservative
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37 QAEGAED 43
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KM SEQUENCE FROM N.A.

KM MEDLINE—21173698; PubMed=11259647;

MEDLINE—21173698; PubMed=11259647;

MACCZ 19089; PubMed=11259647;

MACCZ 19089; PubMed=11259647;

MACCZ 19089; PubMed=11259647;

MACCZ 19080; M.C., Mewton A., Medden J.R.,

MACCZ 19080; M.C., Newton A., Stephens C., Phadke N.D., Ely B.,

MACCZ 19080; M.C., Newton A., S., Gwlnn M.L., Haft D.H.,

MACCZ 19080; M.C., Newton A., S., Gwlnn M.L., Haft D.H.,

MACCZ 19080; M.C., Newton A., S., Gwlnn M.L., Haft D.H.,

MACCZ 19080; M.C., Mewton M.D., Metty J., Berry K.,

MACCZ 19080; M.C., Shapiro L., Fraser C.M.;

MACCZ 19080; M.C., Shapiro L., Fraser C.M.;

MACCZ 19080; M.C., Mewton M.C., Me
                                                                                                                                                                                 Gaps
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Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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                                                                                        Length 2376;
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2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
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Last annotation update)
                                                                                   30.4%; Score 7; DB 5; Len
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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ProDom; PD000621; Cold_shock; 1.
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                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
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Yrenholme K.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
Bradley J.E.;
"Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus
antigens in microfilladermia positive individuals from Esmeraldas
Porvince, Ecuador.",
Parasite Immunol. 16:201-209(1994).
BMBL: S71371: AAC60510.2;
NON TER 98
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P91785;
P91785;
D1-MAY-1997 (TrEMBLrel. 03, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Antigen maltose binding protein (Fragment).
Antigen waltose binding protein (Fragment).
Conchocarca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocarcidae; Onchocarca.
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Miller J.H.;
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26.1%; Score 6; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels
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26.1%; Score 6; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                            Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteaceas;
Thermoproteaceae, Pyrobaculum.
NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009752; AAL62578.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 9492 MW; 22091651B45CADD1 CRC64;
Q82ZR1;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE0124.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
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45 ALAGWL 50
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51 LRPEDG 56
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P91785
AC P9178
DT O1-MA
DT O1-MA
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Search completed: September 11, 2003, 17:55:49 Job time: 22.016 secs

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Result

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Human signal pepti
Human polypeptide
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Human propept
Human secreted/rra
Novel human secret
Human secreted/rra
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Human proproghrell
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Rat des-Gln14-ghre
Rat ghrelin prepro
Porcine des-Gln14-
Porcine ghrelin pr
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Xenopus laevis nuc
Murine APLP! Mus
Human colon cancer
Novel human diagno
Novel human diagno
Drosophila melanog
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                           AAB62649
AAB20101
AAB60511
                                                              ABB78319
AAE23838
AAE15883
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ABU67066
ABU59871
ABU59871
ABU59871
ABU59420
ABU60555
ABU606555
ABU606555
ABU733409
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AAU12392
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AAM40676
ABP08975
AAB60516
AAB60521
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AAR98903
AAG73526
ABG15575
ABG20671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human zsig33-linker peptide #2.
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  11-MAY-2000; 2000US-203300P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JASP/) JASPERS S R. (SHEP/) SHEPPARD P O. (DEIS/) DEISHER T A. (BISH/) BISHOP P D.
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 US2002055156-A1
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  AAE23840;
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AAE23840
  Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
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Protein designated
                                                                                  September 11, 2003, 17:21:03; Search time 23.984 Seconds (without alignments) 152.215 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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AAE15885
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AAE23839
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1 ALAGWLRPEDGGQAEGAEDELEV
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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The invention relates to 28193-11ke periods and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate 251G3 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The 251G33 peptides are used as antigens in the production of antibodies against 251G33 and in assays to identify modulators of 251G33 expression and activity. The anti-251G33 antibodies and antagonists are used to down regulate expression and activity. The anti-251G33 antibodies are also used as diagnostic agents for detecting the presence of 251G331 is amples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or hormones in the pancreas: zsig33-like pobtide. Is used in protein therapy. The present sequence is human zsig33-like peptide. zsig33-linker peptide.
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         contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones
                                                                                                                                zs1g33-like peptides and their corresponding
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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100.0%; Pred. No. 3.6e-11;
11ve 0; Mismatches 0;
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                                                                                        Claim 1; Page 28; 34pp; English.
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Best Local Similarity 100.
Matches 23; Conservative
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(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-443750/47.
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ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

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The invention relates to zaig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones.

The sequences of the invention and their complements are used as mucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The 251G33 perfects may be in need of restorative therapy. The 251G33 and in assays to identify modulators of 251G33 expression and activity. The anti-251G33 antibodies are used to down regulate expression and activity. The anti-251G33 antibodies are also used as diagnostic agents for detecting the presence of 251G33 in samples (e.g. by enzyme linked immunosorbent assays (ELISA). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zaig33-like peptide, zaig33-linker peptide.
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contractility, nutrient uptake, growth hormones and/or secretion digestive/pancreatic enzymes and hormones ^{\rm -}
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Pred. No. 3.6e-11;
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                                                        Claim 1; Page 28; 34pp; English.
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N-PSDB; AAD25760.
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Matches 23; Conserv
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hypoglycaemic preparations containing glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These conjectures are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. E331L peptides, nucleic cids and/or antibodies are useful for treating disorders associated with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and requiation of nutrient absorption. Sequences of the invention are and acids, association of some contractions of the invention are and requiration of nutrient absorption. Sequences of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to zsig33-like peptides (zsi31p) including zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-like peptides. Zsi31p peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and fisolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pitultary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
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                                                                                                                                                                                                                                                                                                      uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises 2s1g33-like peptides -
                                                                                                                                                                                                                                                                       New polypeptides, useful for modulating gastric contractility,
                                                                                                      Deisher TA, Bishop PD;
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100.0%; Pred. No. 3.6e-11;
tive 0; Mismatches 0;
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                                                                                                      Jaspers SR, Sheppard PO,
                                     (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                  The invention relates to zsig33-like peptides (ZS33LP) including
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                                                                 Claim 1b; Page 81; 89pp; English.
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Length 23; Indels

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention and their complements are used as treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide. zsig33-like peptide.
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                                                                                                                                                                                                                                                                                                                                                      ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
contractility, nutrient uptake, growth hormones and/or secretion of
digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; zsig33-like peptide; ZS33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33-linker peptide.
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                                                                                                                                                                                                                                                                   Deisher TA, Bishop PD;
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100.0%; Pred. No. 3.8e-11;
tive 0; Mismatches 0;
/note= "Hydrophilic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE15884 standard; peptide; 24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 28; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zsig33-linker peptide #1.
                                                                                                                                          11-MAY-2000; 2000US-203300P.
                                                                                                     10-MAY-2001; 2001US-0853253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                 Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                         (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                                                                                                                  WPI; 2002-443750/47.
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nes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AA;
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD38239
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                                                                     09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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The invention relates to zsig33-like peptides (zs31LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and casig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and casig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and casig33-linker peptides and nucleic acid molecules encoding such casig33-like peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised in particular such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and cingal infections. Peptides of the invention are used to identify and cingal infections of peptides of the invention are used to identify and cossel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate companies for oral drugs which require fast nutrient action and to hypoglycaemic preparations containing glucose and as adsorption channers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and charmone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These concentrality in vivo and to treat gastrointestinal and growth related diseases. Z331Lp peptides, nucleic contraction of diseative and and/or calial contraction of interaction of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zslg33-like peptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                       /note= "Hydrophilic antigenic site" 7..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deisher TA, Bishop PD;
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Mismatches 0;
                                                                                                                                               /note- "Hydrophilic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 121;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000; 2000US-0569271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaspers SR, Sheppard PO,
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-082982/11.
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                                                                                                                                                                                                                                      W0200187933-A2.
                                                                                                                                                                                                                                                                                                                  22-NOV-2001
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides ovectors and host cells comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide. The peptides caused by a deficiency in growth hormone appression or activity. In particular, they are useful for promoting infant growth due to growth the normone deficiency. The compounds of the invention are useful for promoting infant growth due to growth on accompanying side effects. The present sequence represents a partiturin-type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                              Hosoda H, Matsuo H, Minamitake Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 186-187; 210pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ALAGWLRPEDGGQAEGAEDELEV 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87991 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of infant growth disorders -
                                                                                                                                                                                     23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                              2000WO-JP04907.
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                                                                                                                                                                                                                                                                                                                                                                              Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-159704/16.
N-PSDB; AAF59647.
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                                                                                                                                                                                                                                                                                                                   (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
   WO200107475-A1
                                                                                                                           24-JUL-2000;
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                                                                01-FEB-2001
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      80 X C C C C C C C C C C C X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                               Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy; breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exon-3 deleted preprogheslin and/or a GHS-R Ib protechis or nucleic acids. The antibodies, exon 3-deleted form of preprogheslin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choricorarchinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a cancer cell or tissue for treating prostate, ovarian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 121; DB 24;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herington AC;
                                                                                                                                                                                  Human exon 3-deleted ghrelin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
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AAE33410 standard; Protein; 91
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17-DEC-2001; 2001AU-0009567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2002; 2002WO-AU00582.
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                                                                                                                           (first entry)
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Best Local Similarity 100.0
The 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-111957/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200290387-A1
                                                                                                                                                                                                                                                                                                          cancer; human.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                       02-APR-2003
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                                                             AAE33410;
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RESULT 8

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06-JAN-2000
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                                                                                                                                         Lal P,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                     cids are strongly expressed in stomach lissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal call contractility, secretion of digestive enzymes/acids, gastrointestinal motility, recruitment of digestive carymes/acids, gastrointestinal inflammation, reflux disease and nutrient beborption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify a signal systems and ligands and to produce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                present sequence represents a protein designated Zsig33. The nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation; cardiovascular disease; anticancer; anti-inflammatory; antinicobtal; notropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; carthrobasts; psorthasts; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzhehmer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
                                                                                                                                                                                                   Human polypeptide having homology to motilin, zsig33 - useful e.g to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 121; DB 20;
100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                    Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY87236 standard; Protein; 117 AA.
                                                98WO-US05620.
                                                                        97US-0822897.
97US-0041102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.'
Matches 23; Conservative
                                                                                                                                      Deisher TA, Sheppard PO;
                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                WPI; 1999-070071/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                             N-PSDB; AAX04550
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WO9842840-A1
                                                                                    24-MAR-1997;
                                               23-MAR-1998;
                                                                        24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2000
                       01-0CT-1998
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human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, noctropic, hepatotropic, neuroprotective, cardivascular and antimisthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psortasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischemic heart disease, Alzheimer's, Parkinson's or Huntington's clischemic heart disease, Alzheimer's, Parkinson's or Huntington's clischemic heart disease, microbial or other infections, congestive or ischemic acids can be used for the recombinant production of HSPP, for disease, microbial and mplification assays (for detecting HSPP in standard hybridisation and amplification assays (for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources.
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                                                                                                                                                                                                                                                                                                                                                           Gorgone GA, Corley NC, Guegler KJ, Baughn MR; toung J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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100.0%; Pred. No. 2.2e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 168-169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                           98US-0094983.
98US-0102686.
98US-0112129.
99WO-US14484
                                                                          98US-0090762
                                                                                                                                                                                                                                                                                                                                                                                             Au-Young J,
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                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-160673/14.
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                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ98121
                                                                                                                                                                                                                                                                                                                                                                                                     Akerblom IE,
25-JUN-1999;
                                                                          26-JUN-1998;
                                                                                                                   31-JUL-1998;
01-OCT-1998;
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The invention relates to a method of forming a reversible peptide-
receptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsigi3 peptide (comprising residues 24-37
of AA862649), where the receptor binds to the zsigi3 peptide. The method
is useful for purifying calls, purifying a peptide, stimulating signal
transduction in a call expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of digestive and
modulating secretion in a mammal having a disease associated with abnormal
it secretion of non-zsigi3 proteins. It is useful for modulating growth
hormone secretion in a mammal having a disease associated with abnormal
levels of growth hormone, such as osteoporosis, bone remodeling,
skeletal dysplasia, immune suppression, obesity, growth retardation,
skeletal dysplasia, immune suppression, obesity, growth retardation,
cremodeling a mammal having a disease subscience and mammal having
a metabolic disorder requiring neurological feedback, such as satiety
a metabolic disorder requiring neurological feedback, such as satiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation, glucose absorption and metabolism and neuropathy associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zsig33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-1; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GRS-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .Gaps
                                                                                                                                                                                                       /note- "specifically claimed fragment that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 121; DB 22;
100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 93-94; 111pp; English.
                                                                                                                                                   Location/Qualifiers
24..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB20101 standard; Protein; 117 AA.
                                                                                                                                                                                                                            the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                             99US-0166765.
                                                                                                                                                                                                                                                                                                                                                    2000WO-US32074
                                                                                   G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-355879/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
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                                                                                                                                                                                                                                                                       WO200138355-A2
                                                                                                                                                                                                                                                                                                                                                  22-NOV-2000;
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-1999;
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23;
                                                                                                                                                                                                                                                                                                            31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                     Key
Peptide
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Matches
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AAB20101
ID AAB20
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AC AAB20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic.acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous asystem, such as peripheral nervous system diseases, such as alzahamer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olan XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 121; DB 22;
1 Similarity 100.0%; Pred. No. 2.2e-10;
23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                           2000US-0552317.
2000US-0552317.
2000US-0598042.
2000US-0653450.
200US-0653450.
2000US-0653450.
2000US-0653450.
                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human zsig33 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
N-PSDB; AAI58046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, A
Wang 2, F
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.N.S disorders.
                                                                                                                        WO200153312-A1.
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                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                            19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
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                                                                                                                                                                                                                                                21-JAN-2000;
                                                                                                                                                                                                                                                                                        09-JUL-2000;
                                                                                                                                                                26-JUL-2001
                                          leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
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Best Local
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Fri

23-APR-2001

Homo sapiens

Peptide Protein Peptide 30-JUN-1999;

04-JAN-2001

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promothing infant growth due to growth hormone deficiency. The compounds of the invention are safe with a concompanying side effects. The present sequence represents a ghrein in type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                 Growth hormone secretagogue, GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 121; DB 22;
100.0%; Pred. No. 2.2e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human zsig33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 182; 210pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB78319 standard; Protein; 117
                                                                                                                                                                                                                                                                                23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of infant growth disorders -
                                                                                                                                                                                                                                         24-JUL-2000; 2000WO-JP04907
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
                                                                                                                                                                                                                                                                                                                                                                          (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF59645
                                                                                                                                                    WO200107475-A1
                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see secretagoque receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue. Stimulating contractability in duodenum or jejunum tissue, modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying.
                                                                                SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating
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                                                                                                                                                                                                                                                       /label- Signal_peptide
24..17
24..34
/label- Mature_protein
24..34
/label- SGIP_peptide
/note- "this peptide is claimed in Claim 1"
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                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; 54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000WO-US18306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0345157.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric emptying
                                        Zsig33 protein
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Gaps

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24-APR-2001

DX DX SX

AAB60511;

RESULT 14 AAB60511

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Sequence

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Best Loc Matches

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The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with languages and treatment of diseases associated with the deressed expression by rectifying mutations of deletions in a patient's genome that affect the actifying mutations of SGIP SGIP may also be used as an antigon in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies, agonists and antibodies may also be used as a diagnostic agents for detecting the presence of SGIP in samples.
                                                                                                                                                                                                                                                                                                                                                                  New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 121; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                               Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 39-40; 23pp; English.
                         //note- "signal peptide"
24..119
/note- "mature protein"
Location/Qualiflers
                                                                                                                                                                       30-JUN-2000; 2000US-0608810.
                                                                                                                                                                                                         99US-141592P.
                                                                                                                                                                                                                                                                             Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                            (2YMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                             WPI; 2002-634794/68.
N-PSDB; ABV72214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
                                                                                                                                                                                                         30-JUN-1999;
                                                                                                  US6420521-B1
                                                                                                                                    16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
 Key
Peptide
                                                  Protein
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Search completed: September 11, 2003, 17:25:03 Job time : 23.984 secs

1 ALAGWLRPEDGGQAEGAEDELEV 23

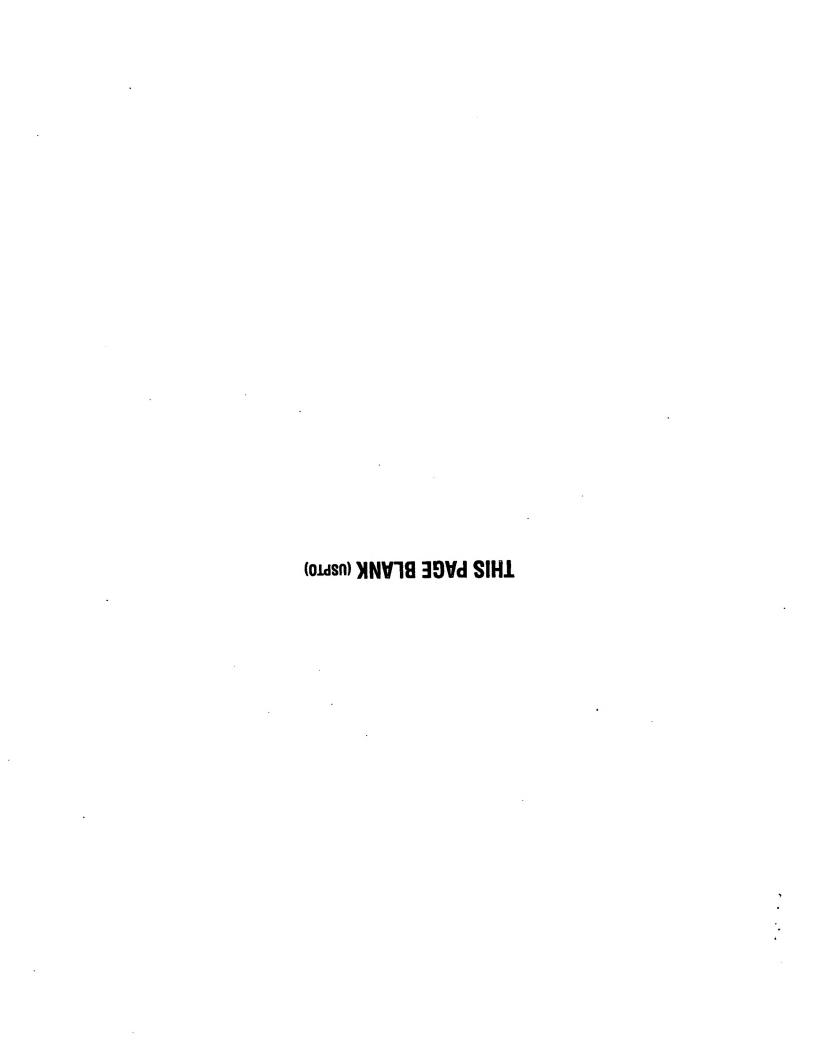
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ALAGWLRPEDGGQAEGAEDELEV 74

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Gaps

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24838, A 21437, A 4, Appl1 27419, A 27950, A

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

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Sednence Sed

Perfect score:

Run on:

Scoring table: Sednence:

Searched:

Database

Result No.

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US-09-394-272-5
US-09-252-991A-20326
US-08-482-304-12
US-08-482-3474-12
US-08-482-347-9
US-09-252-991A-21437
US-09-252-991A-27419
US-09-341-4468-6
US-09-341-4468-6
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US-09-341-4468-8
US-09-341-4468-8
US-09-341-4468-8
US-09-341-4468-8
US-09-252-991A-25523
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COMPUTER: IBM COmpatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09046479; Patent No. 6291653; GENERAL INFORMATION:
APPLICANT: Shepperd, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZYMOGENETICS, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPRAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: ZymoGenetics, Inc.
1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
   1059
1118
1118
1140
1140
1140
1162
1212
1311
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1424
4224
4224
424
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424
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: Se
STATE: V
                                                                                                                                                                                                                                                                                                                                                              US-09-046-479-2
      Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2758, A
Sequence 2778, A
Sequence 17, Appl
Sequence 16, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 23604, A
Sequence 27327, A
Sequence 27327, A
Sequence 27327, A
Sequence 25231, A
Sequence 25231, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Appli
                                                                                                                      (without alignments)
158.243 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                     September 11, 2003, 17:21:03; Search time 6.14973 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-039-198B-10
US-09-252-991A-23604
US-09-252-991A-27327
US-09-252-991A-27327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-822-897C-2
US-09-608-810A-4
US-09-996-243-268
US-09-252-991A-27758
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S-09-252-991A-25921
S-09-252-991A-18853
S-08-704-711A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-339-152A-17
US-08-339-152A-16
US-08-007-999B-3
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-08-704-711A-2
                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                             23
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEV
                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                           US-09-853-253-6
121
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Match Length DB
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3377.66
3377.66
3377.66
377.66
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Gaps

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Length 117; Indels

Ouery Match 100.0%; Score 121; DB 3; Best Local Similarity 100.0%; Pred. No. 6e-11; Matches 23; Conservative 0; Mismatches 0;

MOLECULE TYPE: protein FRAGMENT TYPE: internal

1, Appli 9, Appli 2, Appli 28, Appl

Sequence Sequence Sequence Sequence

-09-211-704A-9

Sequence 1, Appli Sequence 18600, A

US-09-252-991A-18600 US-08-464-340A-4

PCT-US94-08449A-4

Sequence 4, Sequence 4,

```
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                Length 117;
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                                                                                                                                                                                                                                                             Query Match 100.0%; Score 121; DB 4; I
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-996-243-268
; Sequence 268, Application US/09996243
; Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
Grimanddi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION WUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                    1999-06-30
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Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker, Kevin P.
Botstein, David
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fong, Sherman
                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                              ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                          SOFTWARE: Fas
SEQ ID NO 4
LENGTH: 117
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                                                                                                                                                                FEATURE:
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Similarity 100.0%; Pred. No. 6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Squence 4, Application US/09608810A
Patent No. 6420521
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Blahop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
  1 ALAGWLRPEDGGQAEGAEDELEV 23
                      52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                       ; Sequence 2, Application US/08822897C
; Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sawislar, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0
TELECOMUNICATION INFORMATION:
TELECHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                    STREET: 12(
CITY: Seatt
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 23;
                                                                                                                  US-08-822-897C-2
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PRIOR FILING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
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PRIOR PELING DATE: 1998-06-02
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PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
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PRIOR APPLICATION NUMBER: 60/08029
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08030
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PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/08826
PRIOR PLICATION NUMBER: 60/08858
PRIOR PLICATION NUMBER: 60/08858
PRIOR FILING DATE: 1998-06-11
PRIOR PELICATION NUMBER: 60/08861
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PRIOR PELICATION NUMBER: 60/088761
PRIOR PELICATION NUMBER: 60/088761
PRIOR PELICATION NUMBER: 60/088761 R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
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R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512 PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17 PILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-05-07 PRIOR PRIOR

R FFLICATION NUMBER: 60/089001
R PLING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R RILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089947
R PILING DATE: 1998-06-18
R PLING DATE: 1998-06-19
R PLING DATE: 1998-06-19
R PLING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
R RILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R PLING DATE: 1998-06-19
R PLING DATE: 1998-06-20 R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R PILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090435 R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090472

R FILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540

R APPLICATION NUMBER: 60/090542

R PILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24 R APPLICATION NUMBER: 60/090690
R PILING DATE: 1998-06-25
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090695
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R PILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091360
R PILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-01 R FILING DATE: 1998-07-01 R APPLICATION NUMBER: 60/091519 R APPLICATION NUMBER: 60/091626 R APPLICATION NUMBER: 60/091626 R FILING DATE: 1998-07-02 R APPLICATION NUMBER: 60/091633 R FILING DATE: 1998-07-02 R FILING DATE: 1998-07-02 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 PRIOR
PRIOR PRIOR

PRIOR

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Sequence 16, Application US/08339152A
Sequence 16, Application:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Rudolph E.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                  REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.4120000
TELECOMMUTCATION:
TELECHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50;
Pred. No. 1
                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFREENCE/POCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-971-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.38;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.38;
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213 GGRAEGGEDEEEV 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11:11 111 11
233 GGRAEGGEDEEEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
41.3
Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-339-152A-16
                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-339-152A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEG ID NO 27758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-339-152A-17

Sequence 17, Application US/08339152A

Fatent No. 564376

Fatent No. 564376

Fatent No. 564376

FAPLICANT: Tanzi, Rudolph E.

APPLICANT: Tanzi, Rudolph E.

APPLICANT: Kovacs, Dora M.

TITLE OF INVENTION: Methods For Modulating Transcription

TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter

NUMBER NO FEGUROSES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

COUNTRY: DC.

COUNTRY: USA
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Pred. No. 6e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.0%; Score 52; DB 4; Length 233; ilarity 72.7%; Pred. No. 2.7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING ADTE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27758, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                  52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEV 23
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758
                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                           Query Match 100.0°
Best Local Similarity 100.0°
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1011111 : | 102 | 103 | 104 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 105 | 
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nes 8; Conserva
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Matches
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; Sequence 10, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: CROWE, JAMES SCOTT
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; TITLE OF INVENTION: PRECOMBINANT PCR STRATEGY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Goldstein & Fox P.L.L.C.
NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18/08/039,198B
FILING DATE: 29-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,276A
FILLING DATE: 06-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 50; DB 2;
ed. No. 17;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0609.3520003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                  PRIOR DATE: 00 MOO 1330

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,999

PILING DATE: 21-JAN-1993

PRO APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642

FILING DATE: 20-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/930,022 FILING DATE: 17-AUG-1992 ATTORNEY/AGENT INFORMATION: NAME: JORGE A. GOLDSTEIN REGISTRATION NUMBER: 29,021
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: (202)371-2571
                                    1100 New York Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 653 amino acids
amino acid
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Best Local Similarity 76.9
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                      Washington
                                                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-689-276A-3
                                                                           STATE: 1
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                                                        APPLICANT: Wasco, Wilma
APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
TITLE OF INVENTION: THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: SLEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0609.3520002/JAG/GKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bupp, Keith
Magendantz, Margaret
Tanzi, Rudolph
Solomon, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08689276A Patent No. 5891991 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: MASCO, Wilma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 653 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:||| ||| || .
233 GGRAEGGEDEEEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-007-9998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 10; Conserv
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APPLICANT:
APPLICANT:
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Gaps

us-09-853-253-6.rai

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27327
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19723, Application US/09252991A
; Sequence 19723, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; FILE REFERENCE: 107196.18
; FILE REFERENCE: 107196.18
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR APPLICATION NUMBER: US 60/094,190
; RIOR APPLICATION NUMBER: US 60/094,190
; RIOR APPLICATION NUMBER: US 60/094,190
; RIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19723
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                                                                                                                                                                                                                            7; Indels
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33;
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Pred. No. 19;
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                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27327, Application US/09252991A Patent No. 6551795
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181 QPEQGGGEHAQADRPDHLEV 201
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                                                                                                                                                                                                                      0;
                                                                       TYPE: PRT CAGANISM: Pseudomonas aeruginosa US-09-252-991A-29700
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US-09-252-991A-27327
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US-09-252-991A-19723
                                                                                                                                                                                                                                                                                                      3 AGWLRPEDGGQAEGAED 19
                                                                                                                                                                        Query Match 38.8%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.0%;
Best Local Similarity 52.4%;
Matches 11; Conservative ;
     ID NOS: 33142
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Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-27327
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NUMBER OF SEQ I
SEQ ID NO 29700
LENGTH: 283
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APPLICANT:
MATC J. RUBERIELD OF LINVENTION:
APPLICANT:
MATC J. RUBERIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23604
LENGTH: 518
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Petent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION UNMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
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39.7%; Score 48; DB 4; Length 518;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB : Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                 APPLICATION NUMBER: PCT/GB91/01744
FILING DATE: 08-OCT-91
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-252-991A-23604
Sequence 23604, Application US/09252991A
Patent No. 6551795
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412 AGWAQPEPGCGGNGAAERL 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                40.58;
61.58;
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Best Local Similarity 61.5'
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-039-198B-10
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-252-991A-29700
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2 LAGWLRPEDGGQAEGAEDEL 21

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RESULT 15

US-09-252-991A-25921

US-09-252-991A-25921

Sequence 2591, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANTON:

ATTLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25921

LENGTH: 517
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38.0%; Score 46; DB 4; Length 517;
Best Local Similarity 47.6%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 8; Indels
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11 | || || 13 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 1
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25921
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          US-09-989-721-268
US-09-992-598-268
US-09-991-258-268
US-09-991-1181-268
US-09-991-1181-268
US-09-990-43-268
US-09-990-43-268
US-09-997-653-268
US-09-997-653-268
US-09-997-653-268
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US-09-997-653-268
US-09-990-438-268
US-09-990-438-268
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US-09-991-156-268
US-09-997-573-268
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100.0%; Pred. No. 8.3e-10;
iive 0; Mismatches 0;
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US-09-991-854-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-997-601-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09853253;
Patent No. US2002005515641
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TILLE OF INVENTION: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEV 23
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GENERAL INFORMATION: APPLICANT: JASPERS, STEPHEN
Conservative
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Matches 23;
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LENGTH: 23
TYPE: PRT
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 ORGANISM:
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 Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
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Sequence 6, Appli
                                                                                                            September 11, 2003, 17:26:32; Search time 14.0214 Seconds (without alignments) 239.348 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-863-253-4
US-09-989-723-268
US-09-989-723-268
US-09-989-723-268
US-09-989-723-268
US-09-989-723-268
US-09-989-731-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
US-09-991-073-268
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                                                                                                                                                                                                                                                                                                541936 seqs, 145912426 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
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                                                                                 OM protein . protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION CURNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 121; DB 9;
100.0%; Pred. No. 4.2e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09853253
| Patent No. US20020055156A1
| GENERAL INFORMATION:
| APPLICANT: JASPERS, STEPHEN
| APPLICANT: JASPERS, STEPHEN
| APPLICANT: BISHOP, PAUL
| TITLE OF INVENTION: Zsig33-like Peptides
| FILE REFERENCE: 00-30
| CURRENT FILING DATE: 2001-05-10
| PRIOR FILING DATE: 2001-05-11
| NUMBER OF SEQ ID NOS: 28
| SOFTWARR: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/046,479
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: SAWISLAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
98-09-794:987-2
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                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                  STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO:
  CITY: Seattle
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                                                                                                  MEDIUM TYPE:
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100.0%; Pred. No. 8.7e-10;
tive 0; Mismatches 0;
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Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
            APPLICANT: DEISHER, THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 281933-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JASPERS, STEPHEN
APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 281933-11ke Peptides
FILE REFRENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEV 23
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Patent No. US20020055156Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 23; Conservative
SHEPPARD, PAUL
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo saptens
US-09-853-253-4
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) LOCATION: (23)...(23)
US-09-853-253-6
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                                                                                                                                                                                                                                                                                                FEATURE
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R APPLICATION NUMBER: 60/088030
R PILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08326
R APPLICATION NUMBER: 60/08326
R APPLICATION NUMBER: 60/08326
R APPLICATION NUMBER: 60/08327
R FILING DATE: 1998-06-05
R PELING DATE: 1998-06-05
R PAPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088318
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/0883818
R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/0881818
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/0881818
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/0883818
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088818
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088818
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088888
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088888
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088888
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088888
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/0888881
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088881
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088881
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R APPLICATION NUMBER: 60/089512

RR APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090254
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PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE DESTRUCTION Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065310
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PLICATION NUMBER: 60/065710
PRIOR PLICATION NUMBER: 60/065710
PRIOR PLICATION NUMBER: 60/075945
PRIOR PLILING DATE: 1998-02-25
PRIOR PLILING DATE: 1998-02-25
PRIOR PLILING DATE: 1998-03-20
PRIOR PLILING DATE: 1998-03-20
PRIOR PLILING DATE: 1998-03-20
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PRIOR PELLING DATE: 1998-04-28
PRIOR PELLING DATE: 1998-04-28
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08759
PRIOR PELLING DATE: 1998-06-03
PRIOR PELLING DATE: 1998-06-03
PRIOR PELLING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PELLING DATE: 1998-06-04
52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                      RESULT 6
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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Godowski, Paul J.
Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Napier, Mary A.
                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                           Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                       Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan, James
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: P2730PLC62 CURRENT ENLICATION NUMBER: US/09/989,723 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PILICATION NUMBER: 60/049787
PRIOR PILIKG DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELING DATE: 1997-11-13
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PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PAPLICATION NUMBER: 60/08450
PRIOR PELING DATE: 1998-02-26
PRIOR PELING DATE: 1998-02-26
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-07
                                                                                                                                                                                                                                                                                                                       Grimaldi, J. Christopher
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                               Ferrara, Napoleone
Fong, Sherman
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Goddard, Audrey
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Kljavin, Ivar J.
Napier, Mary A.
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                                                        Baker, Kevin P.
Botstein, David
                                                                                                            Desnoyers, Luc
                                                                                                                                       Eaton, Dan L.
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        GENERAL INFORMATION:
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4.2e-09;
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100.0%; Score 121; D
Best Local Similarity 100.0%; Pred. No. 4.2
Matches 23; Conservative 0; Mismatches
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R APPLICATION NUMBER: 60/090444

R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090472

R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

R APPLICATION NUMBER: 60/090536

R APPLICATION NUMBER: 60/090540

R APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090676
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FILING DATE: 1998-06-25
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-02
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Sequence 268, Application US/09989723 Patent No. US20020072092A1

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PRIOR APPLICATION NUMBER: 60/08167
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PRIOR APPLICATION NUMBER: 60/08816
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PRIOR PELLING DATE: 1998 0-6-20
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| PRIOR PAILME DATE: 1998-66-25
| PRIOR PAILME DATE: 1998-67-07
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DR FILING DATE: 1998-06-09
DR APPLICATION NUMBER: 60/088734
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088738
DR PILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/08874
DR FILING DATE: 1998-06-10
DR FILING DATE: 1998-06-10
DR FILING DATE: 1998-06-10
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/08881
DR APPLICATION NUMBER: 60/088824
DR APPLICATION NUMBER: 60/088826
DR FILING DATE: 1998-06-10
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DR FILING DATE: 1998-06-10
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TREATING DATE: 1998-06-11

TREATING DATE: 1998-06-12

TREATING DATE: 1998-06-16

TREATING DATE: 1998-06-17

TREATING DATE: 1998-06-18

TREATING DATE: 1998-06-18

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RELING DATE: 1998-06-19

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RELING DATE: 1998-06-29

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RAPLICATION NUMBER: 60/090254

RELING DATE: 1998-06-22

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RAPLICATION NUMBER: 60/090254

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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/088217
                              LING DATE: 1998-06-0
PRAILOR RATE OF PRAIL OF PRAIL
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APPLICANT: Shang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
GURRENT FILING DATE: 1907-06-16
PRIOR PELICATION NUMBER: 05/09/989,279
PRIOR PELICATION NUMBER: 05/09/987
PRIOR PELICATION NUMBER: 05/09/987
PRIOR PELICATION NUMBER: 06/065311
PRIOR PELICATION NUMBER: 06/065311
PRIOR PELICATION NUMBER: 06/065311
PRIOR PELICATION NUMBER: 06/065310
PRIOR PELICATION NUMBER: 06/08312
PRIOR PELICATION NUMBER: 06/08400
PRIOR PELICATION NUMBER: 06/08020
PRIOR PELICATION NUMBER: 06/08030
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R APPLICATION NUMBER: 60/088031
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-05
FILING DATE: 1998-06-05
FILING DATE: 1998-06-05
                                                                                                                  Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Wattanabe, Colin K.
Williams, P. Mickey
                              Gerritsen, Mary E.
                                                                                      Goddard, Audrey
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APLICANT: Zhang, Zemin Trillian II.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic File REPERENCE: P2730PL65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT APPLICATION NUMBER: 00/06187
PRIOR APPLICATION NUMBER: 00/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 00/065311
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-26
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PRIOR FILING DATE: 1998-04-28
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                                                                 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                         Napier, Mary A.
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ilarity 100.0%; Pred. No. 4.2e-09;
Conservative 0; Mismatches 0;
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                                                                                   R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090540

RR APPLICATION NUMBER: 60/090542

RR APPLICATION NUMBER: 60/09057

R FILING DATE: 1998-06-24

RR FILING DATE: 1998-06-24

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RR APPLICATION NUMBER: 60/09057

RR APPLICATION NUMBER: 60/090676
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RAPPLICATION NUMBER: 60/090678

RELING DATE: 1998-06-25

RAPPLICATION NUMBER: 60/090690

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                 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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Grimaldi, J. Christopher
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Ferrara, Napoleone
FILING DATE: 1998-06-24
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 1
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NR APPLICATION NUMBER: 60/088858

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R APPLICATION NUMBER: 60/088816

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R APPLICATION NUMBER: 60/08816

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514
                             R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08824
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R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
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| PRIOR PELINGO BATE: 1998-06-24
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| PRIOR PELINGO BATE: 1998-06-25
| PRIOR FILINGO BATE: 1998-06-25
| PRIOR PELINGO BATE: 1998-07-02
| PRIOR PELINGO BATE: 1998-07-03
| PRIOR PELINGO BATE: 1998-07

Sequence 268, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION: APPLICANT: Ashkenazi,Avi J. Goddard, Audrey Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. Eaton, Dan L. Ferrara, Napoleone Gerritsen, Mary E. Fong, Sherman Gerber, Hanspeter Kljavin, Ivar J. Napier, Mary A. Baker, Kevin P. Botstein, David Desnoyers, Luc Pan, James US-09-989-731-268 APPLICANT: APPLICANT APPLICANT APPLICANT

Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel

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R APPLICATION NUMBER: 60/08976
R APPLICATION NUMBER: 60/08976
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
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R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089514
R FILING DATE: 1998-06-16
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RAPLICATION NUMBER: 60/089801

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RAPLICATION NUMBER: 60/089908

RETLING DATE: 1998-06-19

RAPLICATION NUMBER: 60/089948

RETLING DATE: 1998-06-19

RAPLICATION NUMBER: 60/089948

RETLING DATE: 1998-06-19

RAPLICATION NUMBER: 60/080952

RETLING DATE: 1998-06-22

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R APPLICATION NUMBER: 60/089598

R PILING DATE: 1998-06-17

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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
                                FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
   APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088861
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                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 2370PLC/O CURRENT APPLICATION NUMBER: 00/049787 CURRENT FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-06-16 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-12 PRIOR PLICATION NUMBER: 60/065186 PRIOR FILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-12 PRIOR PLICATION NUMBER: 60/06531 PRIOR APPLICATION NUMBER: 60/06570 PRIOR FILING DATE: 1997-11-24 PRIOR FILING DATE: 1998-01-25 PRIOR FILING DATE: 1998-01-26 PRIOR FILING DATE: 1998-01-28 PRIOR FILING DATE: 1998-01-01-01 PRIOR P
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PRIOR APPLICATION NUMBER: 60/08803
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-07
PRIOR FILING DATE: 1998-06-07
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR PLING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/08655
R APPLICATION NUMBER: 60/088734
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
                             Williams, P. Mickey
Wood, William I.
Watanabe, Colin K
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                                                                                               Zhang, Zemin
APPLICANT:
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1998-06-24

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CURRENT APPLICATION NUMBER: US/09/989,732 CURRENT FILING DATE: 2001-11-19
                                 CURREW FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PAPLICATION NUMBER: 60/065710
PRIOR FILING DATE: 1997-11-13
PRIOR PAPLICATION NUMBER: 60/081302
PRIOR PAPLICATION NUMBER: 60/08100
PRIOR FILING DATE: 1998-02-20
PRIOR PELLING DATE: 1998-02-20
PRIOR FILING DATE: 1998-02-20
PRIOR PELLING DATE: 1998-05-20
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zenne, Ze
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PRIOR APPLICATION NUMBER: 60/090694
PRIOR PLING DATE: 1998 -06-25
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PRIOR APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998 -07-02
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998 -07-02
PRIOR PELING DATE: 1998 -07-07
                          A APPLICATION NUMBER: 60/090690
BR FILING DATE: 1998-06-25
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BR APPLICATION NUMBER: 60/090694
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BR FILING DATE: 1998-06-26
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FILING DATE: 1998-07-09
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FILING DATE: 1998-07-07
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
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Napier, Mary A.
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Botstein, David
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PRIOR APPLICATION NUMBER: 60/08538
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PRIOR PRINK DATE: 1998 -06.17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PRINK DATE: 1998 -06.17
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICIS
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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Best Local Similarity 100.0%; Pred. No. 4.2
Matches 23; Conservative 0; Mismatches
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091519
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091626
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091983
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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
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Gerber, Hanspeter
Gertitsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
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Stewart, Timothy A.
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Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/065186

997-11-12 WEER: 60/06531 997-11-13 997-11-24 WEER: 60/07594 998-02-20 WEER: 60/07891 998-03-20 WEER: 60/0831 998-03-60/0831 998-03-60/0831 998-05-07 WEER: 60/0831 998-05-07	NUMBER: 60/087699 1998-06-02 1998-06-02 1998-06-03 1998-06-03 1998-06-03 1998-06-04 1998-06-06	WBER: 60 9988-06-0 9988-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0 998-06-0
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PRIOR PLING DATE: 1998-06-24
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R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
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R APPLICATION NUMBER: 60/087607
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R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-04

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R APPLICATION NUMBER: 60/088202

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R FILING DATE: 1998-06-05

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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088876
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089538
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR FILING DATE: 1997-01-11-14
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065250
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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          PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091519
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PRIOR PELING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/09163
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PRIOR APPLICATION NUMBER: 60/09196
PRIOR PELING DATE: 1998-07-07
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Patent No. US20020132252A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Stewart, Timothy A.
FILING DATE: 1998-07-01
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Botstein, David
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RAPPLICATION NUMBER: 60/090472

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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090547

R APPLICATION NUMBER: 60/09057

R APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090696

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090697

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R APPLICATION NUMBER: 60/090695

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R APPLICATION NUMBER: 60/090863
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R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-20
R FILING DATE: 1998-06-22
DR APPLICATION NUMBER: 60/090252
DR FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 67/090349
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APPLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
PHILCATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE OF INVENTION: Acids Encoding the Same

FILE OF INVENTION: Acids Encoding the Same

FILE REPERENCE: P2730PL17

CURRENT APPLICATION NUMBER: US/09/991,163

CURRENT FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

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PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/083322

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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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Patent No. US2002013253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/009901
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PRIOR FILING DATE: 1998-06-19
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PRIOR APPLICATION NUMBER: 60/08021
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PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08032
PRIOR APPLICATION NUMBER: 60/08032
PRIOR PILING DATE: 1998-06-05
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PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
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R FILING DATE: 1998-06-04

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R APPLICATION NUMBER: 60/088029

R APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-07

R APPLICATION NUMBER: 60/088126

R FILING DATE: 1998-06-05

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R APPLICATION NUMBER: 60/088212

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R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
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R FILING DATE: 1998-06-10
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100.0%; Score 121; DB 10;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 23; Conservative 0; Mismatches 0;
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R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/08332
RR FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 268, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein,David
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR PLING DATE: 1998 -07-02
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PRIOR PLING DATE: 1998 -07-03
PRIOR PPLICATION NUMBER: 60/09163
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PRIOR PLING DAT
FILING DATE: 1998-06-19
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100.0%; Score 121; DB 10; 100.0%; Pred. No. 4.2e-09; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 23; Conservative

Gaps ö Indels

Length 117;

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 11, 2003, 17:21:03; Search time 3.32086 Seconds (without alignments)
325.703 Million cell updates/sec
Title: US-09-853-253-6
Perfect score: 121
Sequence: 1 ALAGWLRPEDGGOAEGAEDELEV 23
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Sequence: 1 ALAGWIRPEDGGQAEGAEDELEV 23
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES	Ωï	GHRL_HUMAN	GHRL_RAT	GHRL_PIG	GHRL_MOUSE	GHRL_BOVIN	GHRL_CANFA	NUPL_XENLA	ACYP_BACSU	APP1_MOUSE	NKX1_BISBI	SYM_METKA	NKX1_BOVIN	OPRK_CAVPO	DDX8_ARATH	MM14_PIG	MM14_HUMAN	MM14_MOUSE	MM14_RAT	PAXI_HUMAN	RS9A_SCHPO	HAP5_YEAST	KCF1_HUMAN	PYRG_DEIRA	SNXJ_HUMAN	SPS_VICFA	RGL2_HUMAN	VL1_REOVD	INS_VERMO	TCTP_BRAOL	NK22_MOUSE	CMGA_BOVIN	PKSK_BACSU	SYK_DEIRA
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Query	Match	100.0	74.4	71.9	71.1	59.5	56.2	44.6	42.1	41.3	39.7	39.7	٠.			37.6			37.6			37.2			37.2	37.2	36.8	36.8	36.4	36.4	36.4	36.4	36.4	36.0
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MM14_RABIT SYAP_MOUSE	OPRK_HUMAN SYQ_XANAC	SRCH_RABIT SYV_THETH	KLTK_HUMAN	WFRA_BACSU GLS1_YEAST	INS_LOPPI	IGFB_HUMAN	GRP2_NICSY
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100.0%; Score 121; DB 1; 100.0%; Pred. No. 1.5e-10; tive 0; Mismatches 0;

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117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
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nes 23; Conserv
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Name-1; Synonyms-dhrelin;
Isold-090803-1; Sequence-Displayed;
Name-2; Synonyms-del-Glni4-ghrelin;
Isold-090803-2; Sequence-VSP_003245;
FTM: O-n-octanoylation is essential for activity.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/GhrelinID327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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GO; GO:0005615; C:soluble fraction; TAS.
GO; GO:0005115; F:growth hormone receptor ligand activity; TAS.
GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
GO; GO:0007186; P:G-protein signaling; TAS.
GO; GO:0007186; P:G-protein signaling; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR006738; motilin_assoc.
InterPro; IPR006741; Preproghrelin.
Pfam; PF04644; motilin_assoc: 1.
Pfam; PF04644; motilin_assoc: 1.
ProDom; PD332162; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
ProDom; Cicavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                      hormone secretagogue receptor.;;
Trends Endocrinol. Metab. 12:118 122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the ptulitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                MEDLINE-21203998, PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                     Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
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Missing (in isoform 2).
/FTId=VSP_003245.
L -> M (IN REF. 5).
                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULĂR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                       TISSUE-Stomach;
MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB029434; BAA89371.1; -. EMBL; AB035700; BAB19045.1; -. EMBL; AJ252278; CAB65733.1; -. EMBL; AF26658; AGG10300.1; -. EMBL; EC025791; AAH25791.1; -.
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                                                                                                                 SEQUENCE OF 24-33.
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                                                                                                                                                                                                                                                                                                                               REVIEW.
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hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.
-!- SUBCELLULAR LOCATION.
-!- SUBCELLULAR LOCATION:
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hosoda H., Kojima M., Matsuo H., Kangawa K.; "Purification and characterization of rat des-Gln14-ghrelin, a second endogenous ligand for the growth hormone secretagogue receptor."; J. Biol. Chem. 275:21995-22000(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
in gastrointestinal tissue.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER.26.
STRAIN-Sprague-Dawley; TISSUE-Stomach;
MEDLINE-20067959; PubMed-10604470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21433488; PubMed-11549267;
Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
Matsumoto M., Kojima M., Hayashi Y., Kangawa K.;
Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Structure-activity relationship of ghrelin: pharmacological study ghrelin peptides.";
Biochem. Biophys. Res. Commun. 287:142-146(2001).
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                                                                                                                                                                                                                                                                                                                0907H7, 09ET69;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLAIDN OF SER-26. STRAIN-Spraque-Dawloy; TISSUE-Stomach; MEDLINE-20357315; PubMed-10801861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 279:909-913(2000)
                                                                                                                                                                                                                                                                                   117 AA.
1 ALAGWLRPEDGGQAEGAEDELEV 23
                                          52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-21092536; Pubmed-11162448;
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                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    releasing peptide)
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
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72
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as ing as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreament is (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     Isoid-0907H7-1; Sequence-Displayed;
Name-2; Synonyms-del-Gin14-ghrelin;
Isoid-0907H7-1; Sequence-VSP_003248;
Isoid-0907H7-2; Sequence-VSP_003248;
TISSUE SPECIFICITY: Broadly expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, intestine and adipose tissue.
PTM: O-n-octanoylation is essential for activity. The replacement of Ser-26 by aromatic tryptophan preserves ghrelin activity.
MASS_SPECTROMETRY: MW-3314.9; MW_ERR-0.7; METHOD-Electrospray;
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Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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09GKY5; Q9BDG8; Q9GKY4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
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N-OCTANOATE.
MISSING (in isoform 2).
//FIId=VSP_00348.
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Local Similarity 73.9%; Pred. No. 4.1e-06;
Les 17; Conservative 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
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   Name-1; Synonyms-Ghrelin;
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PROPEP
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GHRL_PIG
SOURCE STREET SERVICE STREET 
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Event-Alternative splicing; Named isoforms-2;
Name-1; Synonyms-Ghrelin;
Isold-O9GKY5-1; Sequence-Displayed;
Name-2; Synonyms-del-Ginl4-ghrelin;
Isold-O9GKY5-2; Sequence-VSP_00347;
-i- PTM: O-n-octanoylation is essential for activity (By similarity).
-i- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalla; Eutherla; Rodentla; Sciurognathl; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
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28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
releasing peptide) (Motilin-related peptide) (M46 protein).
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.---d. No. 1.1e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> P (IN REF. 2; AAK30002).
K -> E (IN REF. 2; AAK30002).
856D3EID6DAB1A76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_003247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHRELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB035704; BAB19049.1; -. EMBL; AF308930; AAK19243.1; -. EMBL; AY028942; AAK30002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB035703; BAB19048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 É
72 K
12785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.98;
65.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01624; GHRELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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A Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Nishi K., Kino B., Kondwa T., Saito T., Saito T., Saito T., Saito T., Saito R., Adota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Ruchi P., Lowis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Sakuli F., Saubli F., Suzuki R., Tomita M., Wagner L., Washio T., Romstein M., Bult C., Futcher C., Fultia M., Gariboldi M., Bronstein M.J., Bult C., Fletcher C., Fultia M., Gariboldi M., Romstein M.J., Bult C., Fletcher C., Fultia M., Gariboldi M., Anonseris P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Assaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Whitnaka P., Mynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A., Washi Yaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isold—09EQXO-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
Fisold—09EQXO-2; Sequence=VSP_0003346;
FISOLS—09EQXO-2; Sequence=VSP_0003346;
FISOUS SPECIFICITY: Mainly expressed in the gastrointestinal tract with higher levels in the stomach, medium levels in the duodenum, jetunum, ileum and colon. Low expression in the testis and brain. Not detected in the salivary gland, pancreas, liver and lung. PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
              MEDLINE-20389976; PubMed-10930375;
Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
"Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";
Gastroenterology 119:395-405(2000).
                                                                                                                                                                                          "Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the, EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Stomach;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21203998; PubMed-11306336;
                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                          Kojima M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIEW
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-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

-!- SUBCELULIAR LOCATION: Secreted (By similarity).

-!- PTM: O-n-octanoylation is essential for activity (By similarity).

-!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                              Pfam: PF04643; motilin_gsscc; 1.
Pfam: PF04644; motilin_ghrelin; 1.
Pfam: PF041644; motilin_ghrelin; 1.
ProDom; PD332162; Preproghtelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHRL_BOVIN STANDARD; PRT; 116 AA.
09BDJ6; 09GKY6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ..5e-05;
... 5; Indels
                                                                                                                                                                                                                                                                                                                                                     N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                        EACB49D2E3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86; DB 1;
Pred. No. 1.5e-05
                                                                                                                                                                                                                                                                                                                                                                                        003246
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.5e
2; Mismatches
       EMBL, AJ243503; CAB46500.1; --
EMBL, AB035701; BAB19046.1; --
EMBL, AB060078; BAB5804.1; --
EMBL, AK008668; BAB25814.1; --
EMBL, AK008660; BAB25934.1; --
MGD, MGI:1930008; Ghrl.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:extracellular; IDA.
InterPro: IPR006737; mctlifn_gasco.
InterPro: IPR006737; mctlifn_ghrelin.
InterPro: IRR005737; mctlifn_ghrelin.
                                                                                                                                                                                                                                                                                                                     GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA; 13207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          71.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 24-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                    Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                     24
52
37
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                      SIGNAL
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Matches
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EMBL; X04766; CAA28460.1; -.
 CAC29156.1;
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 EMBL; AJ298296;
                                                                                                                                       24
52
26
37
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P05221;
                                                                                                                                                               LIPID
VARSPLIC
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                            Query Match
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                                                                                                                                        PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event—Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
IsoId=09BEF8-1; Sequence=Displayed;
Name=2; Synonyms=del-Ginl4-ghrelin;
IsoId=09BEF8-2; Sequence=VSP_00324;
-i- PTM: O-n-octanoylation is essential for activity (By similarity).
-i- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                 BY SIMILARITY.

GHRELIN (BY SIMILARITY).

REMOVED IN MATURE FORM (BY SIMILARITY).

N-OCTANOATE (BY SIMILARITY).

K -> E (IN REF. 2).

F55536DAC5FAS9B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canīs familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomasetto C., Wendling C., Rio M.-C., Poitras P.; "Identification of cDNA encoding WTLRP/ghrelin precursor from dog
                                                                                                                                       Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                       DB 1; Length 116;
                                                                                                                                                                                                                                    59.5%; Score 72; DB 1; Length 116
68.2%; Pred. No. 0.0015;
tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                            117 AA.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE-Gastric fundus;
                                              InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                 Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_grelin; 1.
PRINTS; PR01624; GHRELIN
ProDom; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                        2 LAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                              LECQFDPEVGSQAEGAEDELEI 73
                                                                                                                                                          24 50 GE
51 116 RE
26 26 N-
34 34 K
116 AA; 12792 MW;
                        EMBL; AF350329; AAK18612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ298295; CAC29155.1; -.
                                    BAB19047.1
                                                                                                                                                                                                                                                  Best Local Similarity 68.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9615;
                                    AB035702;
                                                                                                                                                                                                                                                                                                                                                                            GHRL_CANFA (09BEF7;
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                    SIGNAL
                                                                                                                                                                          PROPEP
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de Robertis E.M.;
de Robertis E.M.;
"Cloning of nucleoplasmin from xenopus laevis oocytes and analysis of
its developmental expression.";
Genes Dev. 1:97-107(1987).
--- FONGTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
AND TRANSFERRING THEM TO DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                 GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and cluster of sequences homologous to putative nuclear localization
                                                                                 Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Probom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-87218476; Pubmed-2884102;
Dingwall C., Dilworth S.M., Black S.J., Kearsey S.E., Cox L.S.,
Laskey R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                            N-OCTANOATE (BY SIMILARITY).
Missing (in isoform 2).
/FTId=vSP_003244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3E57FED9D1847CF7 CRC64;
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-i- SIMILARITY: BELONGS TO THE NUCLEOPLASMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
15.SEP-2003 (Rel. 42, Last annotation update)
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InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88112783; Pubmed-3428591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA; 13007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%;
65.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 65.29
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 6:69-74(1987).
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                                                                                                                                                                                                                               Alternative splicing SIGNAL
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9

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Broullet S., Bruschi C.V., Cadawell B., Capano V., Carter N.M.,
A bolizot F., Devine K.M., Dusterhoft A., Bhrlich S.D., Emmerson P.T.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A film K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A film S.Y., Glaser P., Goffeau A., Golighliy E.J., Grandi G.,
A duiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurlta K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
                                                                                    HISTONE BINDING SITE).
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                 DB 1; Length 200;
                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID-1423;
                                                                                                                                                                                                  -> P (IN REF. 2).
A91DD110F2965812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
                                                                                                                 E -> A (IN REF. 2).
V -> I (IN REF. 2).
A -> K (IN REF. 2).
A -> K (IN REF. 2).
S -> P (IN REF. 2).
T -> S (IN REF. 2).
L -> V (IN REF. 2).
MISSING (IN REF. 2).
                                                                                      (PROBABLE
                                                                          Nuclear protein; Phosphorylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                91 AA
                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                 Score 54;
Pred. No.
                                                                                               ۰
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                                        PDB; 1K5J; 21-NOV-01.
InterPro; IPR004301; Nucleoplasmin.
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                       STRAIN-168;
MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97417488; PubMed-9272861;
                                                                                                                                                                                                                                                                                    5 WLRPEDGGQAEGAEDELE 22
                                                            Pfam; PF03066; Nucleoplasmin;
                                                                                                                                                                                                             22023 MW;
                                                                                                                                                                                                                                44.6%;
EMBL; Y00204; CAA68363.1;
PIR; A26169; A26169.
PDB; IEE5; 26-SEP-01.
PDB; IEJY; 24-APR-00.
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 194:191-199(1997).
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27
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72
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80
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200 AA;
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nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                             phosphohydrolase)
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        RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Rescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadala Y.,
Rabato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Rabatori, J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Rabeuchi M., Tanconi E., Takagi T., Takahashi H., Takemaru K.,
Rabeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Rabeuchi M., Tamakoshi A., Vanahashi H., Weitzenegger T.,
Rabato V., Uchiyama S., Vandehol M., Vannier F., Vassarotti A.,
Rahiters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,
Rabato V., Ochikawa H.F., Zumsteln E., Yoshikawa H., Danchin A.;
Rabtills.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - CATALYTIC ACTIVITY: An acyl phosphate + H(2)0 - a fatty acid anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
medina N., mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPL_MOUSE STANDARD, PRT; 653 AA. 003157; 08VC38; 01-OCT-1993 (Rel. 27, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) AMYloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
Solomon F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 1; Length 91; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE ACYLPHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD001884; Acylphosphatase; 1.
PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
PROSITE; PS00151, ACYLPHOSPHATASE_2; 1.
HYPOTHELICAL PROTEIN; HYDTOLASE; COMPLETE PROTECOME.
SEQUENCE 91 AA, 10318 WW; 50795631BF3310F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D86417; BAA22305.1; -
EMBL; 299108; CAB12593.1; -
EMBL; 299108; CAB12593.1; -
EMSP; P00818; 1APS;
Subtilist; BG12947; yflL.
InterPro; IPRO01792; AGVlphosphatase.
Fram; PF00708; AGVlphosphatase.
PRINTS; PRO0112; ACYLPHPHASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LAGWVKNRDDGRVEILAEGPENALQ 54
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate.
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secretase requiretes transcription..;

1. Biol. Chem. 277:44195-44201(2002).

1. FUNCTION: May play a role in postsynaptic function. The C-terminal gamma-secretase processed fragment, ALIDI, activates transcription activation through APBB1 (Fe65) binding. Couples to JIP signal transduction through APBB1 (Fe65) binding. May interact with cellular G-protein signaling pathways. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I.

1. FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of neuronal apoptosis (By similarity).

2. Isubunt: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB and APBA family members, MAPKBIPI and aDB1 (By similarity). Binding to Dabi inhibits its
                                                                                A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.R.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.R.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Doases M.B., Bonaldo M.F., Carrinci P., Prange C.,

R Aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hales J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hales J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Hakesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Scheln J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ō.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99389880; PubMed-10460257; Homayouni R., Rice D.S., Sheldon M., Curran T.; "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22313598; PubMed-12228233;
Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
"Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLUIAR LOCATION: Type I membrane protein. C-terminally processed in the Golgi complex.

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21408156; PubMed-11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Nilkura T., Hiraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.; C.-jun N-terminal Kinase (JNK)-interacting protein-lb/islet-brain-1 Scaffolds Alzheimer's amylold precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96139497: PubMed-8576160;
Beher D., Hesse L., Masters C.L., Multhaup G.;
Regulation of amyloid protein precursor (APP) binding to amypting of the binding sites on APP and collagen type I.";
J. Biol. Chem. 271:1613-1620(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                           TISSUE=Retina;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurosci. 19:7507-7515(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH MAPKBIPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH DAB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLLAGEN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
terminal to the NPXY motif are often required for complete interaction. The NPXY site is also involved in clatherin-mediated
                                                                           -1- PTM: N-glycosylated.
-1- PTM: O-glycosylated.
-1- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
Zinc-binding increases heparin binding. No Cu(II) reducing
activity with copper-binding.
-1- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis, Endocytosis; Cell adhesion; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-LEU.
REQUIRED FOR COPPER(II) REDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPXY MOTIF.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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ZINC-BINDING (BY SIMILARITY).
ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
                                      during neuronal
by caspase-3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y->G: REDUCED BINDING OF APBB1.
P -> PP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
BASOLATERAL SORTING SIGNAL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 1; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMYLOID-LIKE PROTEIN 1.
C30 (BY SIMILARITY).
                                      by caspases
at Asp-623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-SER
                                   PTM: Proteolytically cleaved be apoptosis. Cleaved, in vitro,
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                                                                                                                     EMBL; L04538; AAA37247.1; -.
EMBL; BC021877; AAH21877.1; -.
EMBL; BC051877; AAG562, AAG562, HSSP; PG5067; IMWP.
MGD; MGI:88046; Aplp1.
InterPro; IPR001868; AAPP.
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                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02177; A4_EXTRA; 1
PRINTS; PR00203; AMYLOIDA4
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Best Local Similarity 76.9
Matches 10; Conservative
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644
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464
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653 AA;
                            endocytosis.
                                                                 similarity).
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203
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SIGNAL
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CARBOHYD
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RESULT 10 NKX1_BISBI

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                                                                                                                                                                                                                          JOHN DE TOURING TO LITE INMENT TO NATE A RECORDERS COMPATISON WITH A REVISED DOWN THE REGIST 39:435-440(1998).

- FORWITON: CTILICAL COMPONENT Of the Visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and come photoreceptors and the light-induced lowering of calcium is caused by extrusion via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+) (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-98138491; PubMed-9478004;
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
"CDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                Bison bison (American bison).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYM_METRA STANDARD; PRT; 668 AA.
08TX28;
84FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-trnA synthetase (EC 6.1.1.10) (Methionine--trnA ligase)
                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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300 300
300 AA: 31671 MW; 2BE592DA5AB9781E CRC64;
 300 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.0°
Matches 9; Conservative
                                                                                                                                         Bovinae; Bison.
  STANDARD;
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                                                                                         OR NCKX1
                                                                                                                                                      NCBI_TaxID=9901;
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NKX1_BISBI
046383;
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NON_TER
SEQUENCE
                                                                                                                                         Bovidae;
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Steparev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Antale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Analykh A.G., Koonin E.V., Kozyavkin S.A.,
The complete genome of hyperthermophile Methanopyrus kandleri Av19
an anonophyty of archeal methanopens.,
The Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

-I- FUNCTION: Is required not only for elongation of protein synthesis
but also for the initiation of all mRNA translation through
initiator ERNA(fMet) aminoeylation (By similarity).

-I- CATALYTIC ACTIVITY: ATP + E-methionine + ERNA(Met) - AMP +
Giphosphate + L-methionyl-ERNA(Met).

-I- SUBBNIT: Homodimer (By similarity).

-I- SUBENIT: Homodimer (By similarity).

-I- SUBENIT: Belongs to class-I aminoacyl-tRNA synthetase family.

-I- SIMILARITY: Contains I tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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028139; 046384;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-FEB-2003 (Rel. 41, Last annotation update)
8-FEB-2003 (Rel. 41, Last annotation update)
Schlum/Coatsalum/calclum exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 1) (Retinal rod Na-Ca+K exchanger).
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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HAMAP, MF 00098; fused; 1
InterPro: IPR00495; MetG_Cterm.
InterPro: IPR00495; MetG_Cterm.
InterPro: IPR001412; tRNA synt_1a.
InterPro: IPR002304; tRNA synt_met.
InterPro: IPR002304; tRNA synt_met.
InterPro: IPR002547; tRNA synt_met.
InterPro: IPR002547; tRNA synt_met.
InterPro: IPR002547; tRNA synt_met.
InterPro: IPR00399; met.
ITGRPAMS; TIGR00399; met.
ITGRPAMS; ITGR00399; 
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MEDLINE-21927647; PubMed-11930014;
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53.38;
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LLPEESGESEGODDE 561
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234 23
244 24
857 85
1216 AA;
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nes 9; Conserv
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OPRK_CAVPO
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**MEDLINE=98138491; PubMed=9478004;

**Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;

**Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).

**Controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and cone photoreceptors and the light-induced lowering of calcium is caused by extrusion via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+) (By similarity).

**Controlling the Control in the outer segment in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+) (By similarity).

**Controlling the Control in the outer segment in the exchange for four Na(+) (By similarity).

**Controlling the Control in the outer segment in the exchange for four Na(+) (By similarity).

**Controlling the Control in the outer segment in the exchange for four Na(+) (By similarity).

**Controlling the Control in the outer segment in the exchange for four Na(+) (By similarity).
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                                                                                                                                                                            Primary structure and functional expression of the Na/Ca, K-exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004817; K_NaCaexchang.
InterPro; IPR004481; K_NaCaexchng.
InterPro; IPR004881; K_NaCaexchng.
InterPro; IPR004881; NaCa_Ex; F_NaCaexchng.
InterPro; IPR00481; NaCa_Ex; F_NaCaexchng.
IIGRPAMs; TIGR00927; ZA1904; 1.
IIGRPAMs; TIGR00927; TIGR00367; I.
Vislon; Transport; Antiport; Symport; Calcium transport;
Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
Phosphorylation; Signal; Repeat; Alternative splicing.
Bos taurus (Bovine).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                               Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
                                                                                      SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249; 647-660 AND 1119-1136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note-No experimental confirmation available;
-- TISSUE SPECIFICITY: Retina.
-- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                    SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId-Q28139-2; Sequence-VSP_006159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=028139-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                            from bovine rod photoreceptors.";
EMBO J. 11:1689-1695(1992).
                                                                                                                                MEDLINE-92258377; PubMed-1582405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF025664; AAB88884.1; -. PIR; S20969; S20969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X66481; CAA47108.1;
                                                                                                                                                                                                                                                   TISSUE-Retina;
                                                                                                                   TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-1
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
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CYTOPLASMIC (POTENTIAL).

8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-I-Q-A-G-E-[GA]-G-E-V-{EK}-G.

1 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kie G.X., Meng F., Mansour A., Thompson R.C., Hoversten M.T., Goldstein A., Watson S.J., Akil H.;

"Primary structure and functional expression of a guinea pig kappa opioid (dynorphin) receptor.";

Proc. Natl. Acad. Sci. U.S.A. 91:3779-3783(1994).

-I. FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-INKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform 2).
/FTIG-VSP_006159.
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1; Length 1216;
Pred. No. 44;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 A -> G (IN REF. 2).
131614 MW; 39F149A74D1D0523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (POTENTIAL)
                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Kappa-type opioid receptor (KOR-1).
OPRK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 (APPROXIMATE).
                              POTENTIAL.
                                                                                 POTENTIAL.
                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                           POTENTIAL
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816 GEIQAGEGGEVEGDEDEGEI 835
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STRAIN-Hartley; TISSUE-Brain;
MEDLINE-94224825; PubMed-8170987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GWLRPEDGGQAEGAEDELEV 23
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ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
          SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. Columbia, MEDLINE-97086699; PubMed-8932388; Quigley F., Dao P., Cottet A., Mache R.; "Sequence analysis of an 81 kb contig from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                      PALMITATE (POTENTIAL).

LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

4 FPO53834DBBA623 CRC64;
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15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative per-mRNA splicing factor ATP-dependent RNA helicase.
AT3G26560 OR MFE16.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.8%; Score 47; DB 1; Length 380;
                                                                                                                                                                                                                        EXTRACELLUIAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                                                                      Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPGRRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Phosphorylation; Lipoprotein; Phosphorylation; Lipoprotein; Prosecutive programments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1168 AA.
                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 24:4313-4318(1996).
                                                                                                                                    PIR; A55259; A55259.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 LPGWAEPDGNGSAGPQDEQLE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LAGWLRPEDGGQAEGAEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                         42736 MW;
                                                                                                                         EMBL; U04092; AAA67171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome III
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TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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DDX8_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20277480; Pubmed=10819329;
Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Tabata S.;
Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                clones.";
DNA Res. 7:131-135(2000).

LINE RELEASE OF THE SPLICING OF PRE-MRNA AND MEDIATE
THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (Probable).
SUBCELLULAR LOCATION: Nuclear (Probable).
SUBFAMILY: DDX8/PRP22 OF THE DEAD BOX HELICASE FAMILY. DEAH
SUBFAMILY: DDX8/PRP22 OFTHOLOG.
SUBFAMILY: Contains 1 s1 motif domain.
CAUTION: Ref.1 sequences differ from that shown due to a frameshift in position 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC: 1.
SMART; SM0015; S1: 1.
PROSITE; PS00699; DEAL_ATP_HELICASE; 1.
PROSITE; PS50126; S1: 1.
Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
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28-FEB-2003 (Rel. 41, Last annotation update)
Matrix metalloproteinase-14 precursor (EC 3.4.24.-) (MMP-14)
(Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTWMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MTIMMP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134156 MW; B3632DE4A7A7690C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
DEAH BOX.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S1 MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X98130; CAA66825.1; ALT_FRAME.
EMBL; X97970; CAA66613.1; ALT_FRAME.
EMBL; AB028611; BAB01838.1; -.
HSSP; P05055; 1SRO.
InterPro; IPR001410; DEAD.
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InterPro; IPR001650; Helldase_C.
InterPro; IPR003029; S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 EDGG----QAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00271; helicase_C; 1. Pfam; PF00575; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%;
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Matches 11; Conservative
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538
538
635
777
1168 AA;
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       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMOPEXIN-LIKE.

CYSTEINE SMITCH (POTENTIAL).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

W; B7B2C2C569A96CAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00346; CXSTEINE_SWITCH; 1.
Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE.
MATRIX METALLOPROTEINASE-14.
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.6%; Score 45.5; 45.8%; Pred. No. 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALAGWLRPEDGGQA-EGAEDELEV 23
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001818; Matrixin.
InterPro; IPR006025; Nzn_MTpeptdse.
InterPro; IPR006025; Zn_MTpeptdse.
Pfam; PF00045; Peptidase_M10; 1.
Pfam; PF03333; Peptidase_M10, 1.
                                                                                                                                                                                                                                                                                                                   InterPro; IPR000585; Hemopexin.
                                                                                                                                                                                                                                                                                  EMBL; AF067419; AAD38324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65934 MW;
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SMART; SM00120; HX; 4.
SMART; SM00235; ZNMC; 1.
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Matches 11; Conserv
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SEQUENCE FROM N.A.
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METAL
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Search completed: September 11, 2003, 17:21:45 Job time : 4.32086 secs

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Perfect score: Sequence: Scoring table:

Run on:

Searched:

Database

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091790 deinococcus
090p76 human immun
090p77 human immun
090p77 human immun
09144 bos taurus
091244 bos taurus
091245 human immun
090p55 human immun
090p55 human immun
091252 pseudomonas
091252 pseudomonas
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091253 human immun
090p53 human immun
090p13 human immun
090p11 human immun
090n11 human immun
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Blood:
Strausberg R.;
Interpro; IPR066737; motilin_assoc.
Interpro; IPR066738; motilin_assoc.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
SEQUENCE 117 As; 12929 MW; 2580572EBECB7610 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Q8LRD5
Q9XSP0
Q9GLE4
Q9RZ17
Q90P55
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090NM2
090NL9
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Q93VB3
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078494
090P53
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Q9ETM8
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Q8CH53;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
 PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Query Match
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Q8TAT9;
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Matches
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08ch53 meriones un
0815t3 plasmodium
09445 plasmodium
09445 plasmodium
021724 plasmodium
020p50 human immun
027724 plasmodium
090p50 human immun
091611 pseudomonas
082036 hirame rhab
094189 hirame rhab
095169 capra hircu
09658 caenorhabdi
08xw90 ralstonia s
080n15 human immun
08u638 saroshabdi
080n15 human immun
08u638 saroshabdi
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271.100 Million cell updates/sec
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                                                                September 11, 2003, 17:21:03 ; Search time 21.893 Seconds
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                   Compugen Ltd
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                           830525 segs, 258052604 residues
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                                              OM protein - protein search, using sw model
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                                                                                                     US-09-853-253-6
121
1 ALAGWLRPEDGGQAEGAEDELEV
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QBCH53
QBCH53
QBUA45
QBLNL6
QBLNL6
Q27724
Q90P50
Q90P50
Q90L89
Q90L89
Q9NC38
Q9NC38
Q9NC38
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sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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Maximum Match 100%
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sp_bacteriap:*
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sp_bacteria:*
sp_fung1:*
sp_human:*
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Maximum DB seq length: 200000000
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sp_rodent:*
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                            Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                                                                                            Ishli H.;
"Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF442491; AAO06965.1; -.
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                                          Meriones ungulculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                                                                                                                                           ö
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NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%; Score 59; DB 5; Length 1208; 52.6%; Pred. No. 8.2; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                            76.0%; Score 92; DB 11; Length 11
73.9%; Pred. No. 1.3e-05;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014846; AAN36207.1; -. SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;
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Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-3D7;
MEDLINE-22255705; PubMed-12368864;
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                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 73.9 Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-type ATPase, putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Matches 10; Conserv
                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                NCBI_TaxID=10047;
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                                                                                                           Meriones
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Q9U445;
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                                                                                                                                                                                                                          "Expression and Functional Characterization of a Plasmodium falciparum
                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 276:10782-10787(2001)
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN—cv. Nipponbare;
McComble W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBa0071120, from chromosome 10, complete sequence.";
Submitted (JUL-2002) to the ENBL/GenBank/DDBJ databases.
EMBL; AC074355; AAM74240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                           Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
                                                                                                           SEQUENCE FROM N.A.
MEDLINE-21179120; Pubmed-11145964;
Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Sukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                             Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0119; CATATPASE.
TICREAMS; TICR01404; ATPASE_P-type; 5.
PROSITE; PS00154; ATPASE_E1_E2, 1.
ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SEQUENCE 1264 AA; 140261 MW; 6381428B18433640 CRC64
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SEQUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006068; Cation_ATPase_C.
InterPro; IPR004014; Cation_ATPase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00689; Cation_ATPase_C; 1. Pfam; PF00690; Cation_ATPase_N; 1. Pfam; PF00122; E1-E2_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF203980; AAF17245.1; -.
HSSP; P04191; 1EUL.
InterPro; IPR001757; ATPGSG_E1-E2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00702; Hydrolase; 1
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Best Local Similarity 52.6
Matches 10; Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
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                                                  NCBI_TaxID=5833;
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OSJNBA0071120.2
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1131 WCRPKDNKTSDGYNDELE 1148
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                                                                                                                                        / Match 43.8%;
Local Similarity 50.0%;
nes: 9; Conservative
                     HATPASE
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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PRINTS; PR00119;
PRINTS; PR00120;
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Q90P50;
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Matches
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Q916L1
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"Analysis of a cation-transporting ATPase of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 78:1-12(1995).
1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
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MICKLE D.C.:
MICKLE D.C.:
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF370911: AAK66310.1: -
INTERPROPTO: FOR120: -
Fram: PF00516; GP120: 1.
AIDS: Coat protein; Glycoprotein.
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.8%; Score 53; DB 15; Length 202; Best Local Similarity 45.5%; Pred. No. 9.1; Matches 10; Conservative 3; Mismatches 9; Indels
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                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro: IPR006068; Cation_ATPBSE_C.
InterPro: IPR006069; Cation_ATPBSE_N.
InterPro: IPR00693; H_ATPBSE_N.
InterPro: IPR00695; H_ATPBSE_C.
Pfam; PF00699; Cation_ATPBSE_C; 1.
Pfam; PF00612; E1-E2_ATPBSE_N; 1.
Pfam; PF001702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
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                                                                                                                                                             PRT;
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                                      53 AGWIETEDGSDEESDESDSEV 73
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                 3 AGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPASES).
1; U39298; AAC47167.1; -.
2; P04191; 1EUL.
                                                                                                                                                             PRELIMINARY;
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090P58
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STRAIM-ATC. 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Goltty L., Tolentino E., WestDrock Wadman S., Yuan Y., Garber R.L., Goltty L., Tolentino E., WestDrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lin R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
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Pseudomonadaceae; Pseudomonas.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR70919; AAK66318.1; -.
InterPro: IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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                                                                                                                                                      Length 1228;
                                                                                                                                                                                                                       6; Indels
TIGRFAMS; TIGR01494; ATPase_P-type; 5.
PROSITE; PS00154; APPASE_BL_E2; 1.
ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SEQUENCE 1228 AA; 135989 WW; 32C3CF0324964CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AA; 22550 MW; 6CAF6C460A9BA517 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                      Score 53; DB 5
Pred. No. 61;
3; Mismatches
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InterPro; IPR004902; Rhabdo_ncap_2.
Pfam; PF03216; Rhabdo_ncap_2; 1.
SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                             -!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 52; DB 16; Length 232; 72.7%; Pred. No. 15;
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                                                                                                                                                     EMBL; AE004466; AAG03668.1; -.
InterPro; IPR001845; HTH_ArsR.
Pfam; PF011022; HTH_5; 1.
PRINTS; PR00778; HTHARSR.
SMART; SMO0418; HTH_ARSR.
DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 232 AA; 24440 MW; E3C29187694CF936 CRC64;
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Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;
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Of H.K., Chol T.J.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104985; AAF14116.1; -.
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Rhabdoviridae; Novirhabdovirus.
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Last annotation update)
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Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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(TrEMBLrel. 07, L
(TrEMBLrel. 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 75. v.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 72.7
nes 8; Conservative
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01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                 REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q82036;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BECK C.L., Fahlke C., George A.L.;

Molecular basis for decreased muscle chloride conductance in the
                                                                                                                                                                                                                                                                                                                                    Skeletal muscle voltage-gated chloride channel gclc-1 (Fragment). Capra hircus (Goat).
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                        DB 12; Length 392;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  977 AA; 107894 MW; 1E462B3CB307A148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myotonic goat.";
Proc. Natl. Acad Sci. U.S.A. 93:11248-11252(1996).
EMBL; U60275; AAC48666.1;
InterPro: IPR001807; Cl-channel_volt.
InterPro: IPR001807; Cl-channel_volt.
InterPro: IPR005829; Sug_transporter.
Pfam; PF00571; CBS; Zog_transporter.
Pram; PF00571; CBS; Zog_transporter.
Pram; PR00764; voltage_CLC; I.
PRINTS; PR00762; CLCHANNEL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; I.
                                                                                                                                                                                                                                                       095169;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.0%; Score 52; DB 6; 62.5%; Pred. No. 67;
                                                                                                                                                                                                                                       977 AA.
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                  43.0%; Score 52; DB 75.0%; Pred. No. 26; ative 1; Mismatches
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Query Match
Query Match
Best Local Similarity 75.00,
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                                                                                                  9 EDGGQAEGAEDE 20
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                                                                                                                                                                                                                                         PRELIMINARY;
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Nickle D.C.;
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
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Bacteria: Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 436;
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                     "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                               MCMurray A.A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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Pfam: PF01402; HTH_4; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AA; 49496 MW; E0C71263BC580EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
101-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein RSc2585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%; Score 51.5; D
Hlarity 52.9%; Pred. No. 34;
Conservative 5; Mismatches
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EMBL: 275540; CAB70221.1;
EMBL: 275540; CAB70221.1;
EMBL: 275540; CAB70221.1;
EMBL: 275540; CAB70215.1;
EMBL: 275640; CAB70215.1;
EMBL: 275640; CAB70215.1;
EMBL: 275640; CAB70215.1;
InterPro: IPR001132; Dwarfin.
InterPro: IPR001132; Dwarfin.
InterPro: IPR00136; MH2: 1.
SMART; SM00223; DWA: 1.
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MEDLINE-21681879; Pubmed-11823852;
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169 WIRPETNGGDDDGSEDK 185
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Matches 9; Conserv
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090NL5;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 19, Last sequence update)
DE Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viru
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104, App 104, Appl 14, Appl 14, Appl 216,77, A 325, Appl 234, App 31, Appl 31, Appl

Sequence Seq

Title: Perfect score:

sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Database :

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US-08-428-488-13
US-08-981-739-104
US-08-918-739-104
US-08-975-080-11
US-08-975-080-11
US-09-318-35-5646
US-09-251-991A-21677
US-09-489-847-335
US-09-048-502-3
US-09-048-502-3
US-09-048-502-3
US-09-048-502-3
US-09-048-502-3
US-08-01-855-31
US-08-510-6468-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                              US-09-107-532A-6022
                                                                                                                                                                                                         US-09-048-502-1
US-09-634-238-275
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                              RESULT 1
US-09-046-479-2
Sequence 2, Application US/09046479
Fatent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: sir
  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
 sequence 18, Appl
Sequence 4, Appli
Sequence 18, Appl
Sequence 18, Appli
Sequence 4, Appli
Sequence 27031,
Sequence 27031, Appli
Sequence 2861, A
Sequence 18, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 18, Appli
Sequence 18, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 3033, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 18, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
                                                                                                  (without alignments)
123.627 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                   September 11, 2003, 17:48:42; Search time 40.0428 Seconds
                                                                                                                                                                1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                       1: /cgg2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-822-8976-2

US-09-608-810A-4

US-09-608-810A-2

US-09-134-001C-3033

US-09-134-001C-3033

US-09-134-001C-3033

US-09-134-001C-3033

US-09-134-001C-3033

US-09-135-115-18

US-09-135-115-18

US-09-135-115-18

US-09-135-115-18

US-09-135-115-18

US-09-252-991A-27032

US-09-252-991A-27033

US-09-252-991A-27033

US-09-252-991A-27033

US-09-252-991A-27033

US-08-459-165-3

US-08-459-165-3

US-08-459-165-3

US-08-459-165-3
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                          OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                 US-09-853-253-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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Match Length
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100.0
100.0
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Score

Result No.

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Gaps

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Ö DB 3;

Query Match 100.0%; Score 117; DB 3; Best Local Similarity 100.0%; Pred. No. 1e-109; Matches 117; Conservative 0; Mismatches 0

Sequence Seguence

Sequence Sequence

US-09-582-096-9

Length 117; Indels

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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
              1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                        Sequence 2, Application US/08822897C Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET UNDBER: 37,438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                   CITY: Seat
STATE: WA
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US-08-822-897C-2
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61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT APPLICATION NUMBER: US/09/996,243
PRIOR APPLICATION NUMBER: G0/049787
PRIOR PELING DATE: 1997-06-16
PRIOR FILING DATE: 1997-0-16
PRIOR FILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/062186
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APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Delsher Theresa A.
APPLICANT: Delsher Theresa A.
TITLE OF INVENTION: SGIP PEPTIDES
TITLE OF INVENTION: SGIP PEPTIDES
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ FOR Windows Version 3.0
SSOFTWARE: FastSEQ FOR Windows Version 3.0
SSOFTWARE: TITLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268, Application US/09996243
Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy A.
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Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.C
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kljavin, Ivar J.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botstein, David
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-996-243-268
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-21
PRIOR PLING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR PELICATION NUMBER: 60/075945
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-05-28
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08819
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998 PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08858
PRIOR PILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08861
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-11 PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16 FILING DATE: 1997-11-12

NR APPLICATION NUMBER: 00/090349

NR APPLICATION NUMBER: 60/090355

NR APPLICATION NUMBER: 60/090355

NR APPLICATION NUMBER: 60/090429

NR APPLICATION NUMBER: 60/090431

NR APPLICATION NUMBER: 60/090434

NR APPLICATION NUMBER: 60/09044

NR APPLICATION NUMBER: 60/090445

NR APPLICATION NUMBER: 60/090540

NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090578

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090678

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090690

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090690

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090690

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090691

NR FILING DATE: 1998-06-25

NR APPLICATION NUMBER: 60/090691 RELILING DATE: 1998-06-16

REPLICATION DATE: 1998-06-16

REFLING DATE: 1998-06-17

REPLICATION UNBER: 60/089532

REPLICATION NUMBER: 60/089598

RELILING DATE: 1998-06-17

REPLICATION NUMBER: 60/089599

REPLICATION NUMBER: 60/089599

REPLICATION NUMBER: 60/089599

REPLICATION NUMBER: 60/089599

REPLICATION NUMBER: 60/089601

REPLICATION NUMBER: 60/089601

REPLICATION NUMBER: 60/089901

REPLICATION NUMBER: 60/089901

REPLICATION NUMBER: 60/089908

REPLICATION NUMBER: 60/089918

REPLICATION NUMBER: 60/0802518

REPLICATION NUMBER: 60/0902518

REPLICATION NUMBER: 60/0902518

REPLICATION NUMBER: 60/0902518

REPLICATION NUMBER: 60/090349

REPLICATION NUMBER: 60/0903518

REPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 PPRIOR REPRESENTATION OF PRINCIPLE STREET, STR PRIOR PRIOR

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                                                                                                                                                                                                                                                              Length 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl Henrik
APPLICANT: HELDIN, Carl Henrik
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 502;
                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: The PC-DOS/MS-DOS
SOFTWAREN TAPLICATION DATA:
APPLICATION NUMBER: US/08/481,337A
FILING DATE: 02-JUN-1995
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEYERS, Thomas C.
REGISTRATION NUMBER: 36,989
REPERENCE/DOCKFT NUMBER: 36,989
REPERENCE/DOCKFT NUMBER: 36,789
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 8:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 7; DB 2;
100.0%; Pred. No. 53;
.ive 0; Mismatches
                                                                                                                                                                                                                                                          Ouery Match
6.0%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testa, Hurwitz & Thibeault
                  PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 3033
LENGTH: 442
                                                                                                                                                                                             ORGANISM: Staphylococcus epidermidis US-09-134-001C-3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08481337A Patent No. 5863738
1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 502 amino acids
amino acid
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Matches 7; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Boston
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189 DGGQAEG 195
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STATE: MA
COUNTRY: US
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                                                                                                                                                                           TYPE: PRT
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
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100.0%; Pred. No. 0.00016;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 117; DB 4; Best Local Similarity 100.0%; Pred. No. 1e-109; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Stephen R.
APPLICANT: Dalspers, Stephen R.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 1099-06-30
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
           PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09608810A; Patent No. 6420521
PRIOR FILING DATE: 1998-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.4
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-810A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 11
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Sequence 18, Application US/09395115

Sequence 18, Application US/09395115

Patent No. 6271365

GENERAL INFORMATION:
APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
APPLICANT: Franzen, Petrari Yamashita, Hiddetoshi; Heldin, Carl-Henrik TITLE OF INVENTION: Activin Receptor-Like Kinase Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 7; DB 3;
100.0%; Pred. No. 53;
.ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCTYCB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 28-May-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 3-August-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 3-August-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 15-October-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 15-October-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37,003
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TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                           SSEE: Felfe & Lynch
F: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                  STATE: New
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
       JS-09-395-115-18
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                                        Sequence 18, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIXAZONO, KOHel
TEN DIJKE, Petra
FRANZEN, Petra
FRANZEN, Petra
FRANZEN, Garl-Henrik
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
AND THEIR USE
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: NO. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: NO. 6207814ember 17, 1992
PILING DATE: NO. 6207814ember 17, 1992
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: August 3, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: OCLOBER 15, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: LUD 5298.1
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100.0%; Pred. No. 53;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-382-256-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 752-5958 INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 502 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                  NUMBER OF
                      -09-382-256-18
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133 TVCSLLL 139

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RESULT

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APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein

US-08-436-265-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-679-187-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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Sequence 18, Application US/08436265

Sequence 18, Application US/08436265

SENERAL INFORMATION:

APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;

APPLICANT: Arazen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use VORESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CORPERS New York City

STATE: New York City

STATE: New York

ZIP: 10022

COMPUTER: EDISKette, 3.5 inch, 360 kb storage

COMPUTER: IBM.

COMPUTER: IBM.

COMPUTER: IBM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                 STATE: MA CambridgePark Drive STATE: MA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                          GENERAL INFORMATION:
APPLICANT: WORNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. SCOTT
APPLICANT: TAWAJI, No. 6291206oru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; 1
Pred. No.
                               Sequence 4, Application US/08123934A
Patent No. 6291206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEPHOR: 617 876 1170
TELEPHOR: 617 876 1170
SEQUENCE CHARACTERISTICS:
LENGTH: 502 anino acids
TYPE: amino acids
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Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
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RESULT 10
US-08-123-934A-4
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Patent No. 6331621

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik

TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins

TITLE OF ENGENCES: 29

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
FILING DATE: 30-October-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 17-No. 6316217ember-1992
APPLICATION DATA: 8-March-1993
PRIOR APPLICATION DATA: 8-March-1993
FILING DATE: 28-May-1993
FILING DATE: 28-May-1993
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA: APPLICATION D
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100.0%; Pred. No. 53;
1ve 0; Mismatches
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100.0%; Pre-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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Length 502;
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TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
TITLE OF INVENTION: SURPACE RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ 6
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%; Score 7; DB 5; Best Local Similarity 100.0%; Pred. No. 53; Matches 7; Conservative 0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10080
FILING DATE: HEREWITH
                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application PC/TUS9505467; GENERAL INFORMATION:
                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-826
INFORMATION FOR SEC ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/CDOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    : 502 amino acids
amino acid
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-05467-8
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GENERAL INFORMATION:
APPLICANT: GENETICE INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
           APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-0CT-2000
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-0ctober-1995
FILING DATE: 30-0ctober-1995
FILING DATE: 30-0ctober-1995
FILING DATE: 17-No. 6331621ember-1993
APPLICATION NUMBER: PCT/CB93/02367
FILING DATE: 17-No. 6331621ember-1993
APPLICATION DATA: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 931344.5
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-0ctober-1993
APPLICATION NUMBER: 37,003
RECISTRATION NUMBER: 37,003
RECISTRATION NUMBER: 37,003
RECISTRATION NUMBER: 27,003
RECISTRATION NUMBER: 27,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELLECOMMUNICATION NUMBER: LUD 5298
TELEBROWER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-679-187-18
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RESULT 15
US-09-252-991A-27032
Squence 27032, Application US/09252991A
Federat No. 6521795
GENERAL INFORMATION:
APPLICANT MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27032
MATCH FILING DATE: 1998-07-27
MATCH FILING DATE
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Query Match 6.0%; Score 7; DB 5; Length 502; Best Local Similarity 100.0%; Pred. No. 53; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT : ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27032
                                                                                                                                                                                                                                                                             133 TVCSLLL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DGGQAEG 67
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22 DGGQAEG 28
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Novel Novel Human Novel Human Human

Human preproghrell Human PRO1066 poly Human PRO polypept Membrane-bound pro Human PRO1066 poly

Human

Human

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Word size :

Database

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Human Human Human Human Human

polypeptide
des-Gin14-gh
des-Gin14-gh
des-Gin14-gh
des-Gin14-gh
ghrelin pept
zsig33-beta
zsig33-beta
ghrelin pept

Human Human Human Human

Human Human

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2sig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
1..23
...6.e. "signal peptide"
24..117
/note- "mature protein"
                                                                                 ABUS 8977
AAE33409
ABU10892
AAY66708
AAU12392
AAU12392
AAU12392
AAU12392
AAB60517
AAE39038
AAE219032
AAE219032
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AAE19021
AAE19027
AAE19028
AAE19029
AAE19030
                                                 ABU59420
ABU60555
ABU58046
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AAE19034
AAE19035
                                                                                                                                                                                                                                                                                                                                                           AAE19036
AAE19037
AAE19038
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 98WO-US05620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0822897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein designated zsig33
07-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1997;
24-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1998;
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                                                                                                                                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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 Human signal pepti
Human polypeptide
Human zsig33 polyp
Zsig33 protein. H
Human ghrelin prep
Amino acid sequenc
Human zsig33 prote
Human zsig33 prote
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                                                                     September 11, 2003, 17:27:22; Search time 123.257 Seconds (without alignments) 150.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                       1 MPSPGTVCSLLLLGMLWLDL.......LGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                     1107863
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            1107863 seqs, 158726573 residues
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                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                   - protein search, using sw model
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AAX87236
AAM38890
AAB62649
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AAB60511
AAB78318
AAE15883
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
                                                                                                                US-09-853-253-2
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(ZYMO) ZYMOGENETICS INC

117 117 117 117 117 117

Result No.

98US-0112129

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11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatrotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                       Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 117; DB 20; Length 117; 100.0%; Pred. No. 2.3e-101; ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                 Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY87236 standard; Protein; 117 AA
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98US-0094983.
98US-0102686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 117; Conservative
   Sheppard
                                                             WPI; 1999-070071/06.
N-PSDB; AAX04550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200000610-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
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   Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-2000
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NAME TO SECOND T
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characteries and peptide-contenting process. Associated with leptes have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can can eused in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation of HSPP are acceptive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, crohn's disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP concleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring). In gene therapy, as antisense, cripozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to matgonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic cantagonists, in competitive drug screens, and for purification of HSPP con natural sources.
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                                                                                         YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to AA298242 encode AAY87224 to AAY87357 which represent the
                                                                                                                                                                                                                                                                                                                                                                                                     New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 168-169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM38890 standard; Protein; 117 AA
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(INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                      WPI; 2000-160673/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117 AA;
                                                                                         Lal P, Tang YT,
Akerblom IE, Au-
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ98121
                                                                                                                                                                                  Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA298109
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zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pencreatic; human; insulin-like growit procestor-l; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
                                                                                                                                     /note= "specifically claimed fragment that binds to
    the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                   Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                      Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 93-94; 111pp; English.
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                           22-NOV-2000; 2000WO-US32074.
                                                                                                                                                                                                                                                    99US-0166765.
                                                               G-protein coupled receptor
                                                                                                                                                                                                                                                                                                      Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Nes 117; Conservative
                                                                                                                                                                                                                                                                             ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                              WPI; 2001-355879/37.
N-PSDB; AAF83678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
                                                                                                                                                                          WO200138355-A2
                                                                                                                                                                                                                                                                                                      Sheppard PO,
                                                                                                                                                                                                                                                    22-NOV-1999;
                                                                                       Homo sapiens
                                                                                                                                                                                                   31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tches
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, mamunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous Injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous alocalised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral socierosis, and ShyDrager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ssays for receptor activity, arthritis and inflammation, leukaemias and N.S. disorders.

The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                   Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 117; DB 22; Length 117; 100.0%; Pred. No. 2.3e-101; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                    Qian XB,
Yang Y,
                                                                                                                                                                                                                                                  Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                               Wehrman T, Xu C, Xue AJ
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB62649 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                  Liu C, Asundi V,
Wang Z, Wehrman T,
                                                                                                                                                2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                                                                                     2000US-0693036
2000US-0727344
                                                                                    2000WO-US34263
                                                                                                             2000US-0488725
                                                                                                                        2000US-0552317
2000US-0598042
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                                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47
N-PSDB; AAI58046.
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Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                           Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                   WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification
           Homo sapiens
                                                                                    26-DEC-2000;
                                                                                                                                                                                                 29-NOV-2000;
                                                                                                                                                 19-JUL-2000;
                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                      -OCT-2000;
                                                                                                            21-JAN-2000;
                                                            26-JUL-2001
                                                                                                                                      09-JUL-2000
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                                                                                                                                                                                                                                                                            Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                   Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assays
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Bishop PD;

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The invention relates to a method of forming a reversible peptide-
receptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (Comprisibility and acalay)
of AAB62649), where the receptor binds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
cansiderion in a cell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of digestive and
parcreatic enzymes and hormones, secretion of insulin-like growth factor
c. secretion of non-zsig33 proteins. It is useful for modulating growth
common secretion in a mammal having a disease associated with abnormal
evels of growth hormone, such as osteoporosis, bone repair, bone
remodeling, low osteoblast levels, cartilage repair and remodeling,
skeletal dysplasia, immune suppression, obesity, growth retardation,
skeletal dysplasia, immune suppression, obesity, growth retardation,
catabolic responses after surgery, cachexia, protein loss,
dwarfism, wound healing and ovulation induction, treating a mammal having
a metabolic disorder requiring neurological feedback, such as satilety
capulation, glucose absorption and metabolism and neuropathy-associated
gastrointestinal disorders, and stimulating glucose-induced insulin
celease in a mammal. The present sequence represents the human zsig33
polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
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Query Match
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RESULT 6
               AAB6051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jedunum tissue. Amodulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying.
                                                                                                                  SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                              /label- SGIP_peptide
/note- "this peptide is claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 117; DB 22;
100.0%; Pred. No. 2.3e-101;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                24.117
/label- Mature_protein
24.34
/label- SGIP_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deisher TA,
                                                                                                                                                                                                             l..23
/label- Signal_peptide
                                                                                                                                                                                                  Location/Qualiflers
           AAB20101 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; 54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000WO-US18306
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Tes 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-123010/13.
N-PSDB; AAF30033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastric emptying
                                                                                                                                               :herapy; human.
                                                                                         zsig33 protein.
                                                                                                                                                                                                                                                                                                                    WO200100830-A1
                                                                                                                                                                        Homo sapiens
                                                               23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                               04-JAN-2001
                                   AAB20101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duery Match
                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                 Peptide
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Matches
AAB20101
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a local compasses the unmodified peptides; the DNA encoding the peptides comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising are useful for treating and/or diagnosing diseases of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with an accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                      Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide compounds which induce growth hormone secretion elevate cell calcium concentrations, useful in treatment and of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuo H, Minamitake Y;
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100.0%; Pred. No. 2.3e-101;
ive 0; Mismatches 0;
                                                                                                                                                                                         Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 182; 210pp; Japanese.
AAB60511 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0210002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2000; 2000WO-JP04907
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                   growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200107475-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1999;
                                                                                                                         24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                             domo sapiens
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                                                            AAB60511;
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RESULT

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2SIG33-Like peptides and polynucleotides, useful for modulating gastric
contractility, nutrient uptake, growth hormones and/or secretion of
digestive/pancreatic enzymes and hormones -
                                                                                                                  Human, zsig33-like peptide, gastric contractility, nutrient uptake,
growth hormone; digestive enzyme; restorative therapy; gene therapy,
protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                                                                                                                                                      10-MAY-2001; 2001US-0853253.
                                                                                                                                                                                                                                                                                                                       11-MAY-2000; 2000US-203300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                      JASPERS S R.
SHEPPARD P O.
DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-443750/47.
N-PSDB; AAD38238.
                                                                                                                                                                                                                                                                                                                                                                                                         (BISH/) BISHOP P D.
                                                                                                                                                                                                                    US2002055156-A1.
                                                                                   Human zsig33
                                                                                                                                                                                      Homo sapiens.
                                                  10-SEP-2002
                                                                                                                                                                                                                                                     09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                   AAE23838;
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                                                                                                                                                                                                                                                                                                                                                      (JASE/)
                                                                                                                                                                                                                                                                                                                                                                      SHEP
                                                                                                                                                                                                                                                                                                                                                                                         (DEIS/)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with the inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antigonists may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used dariance of SGIP in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Short Gastrointestinal Peptide, which has homology to motilin, mestil for preventing, diagnosing and treating gastrointestinal
                                                                                                                                                  Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 117; DB 23;
100.0%; Pred. No. 2.3e-101;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Columns 39-40; 23pp; English.
                                                                                                                                                                                                                                                               24..119 //note= "mature protein"
                                                                                                                                                                                                                                   1..23
/note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deisher TA,
                                                                                                                 Amino acid sequence of a human zsig33
                                                                                                                                                                                                                    Location/Qualifiers
               ABB78319 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000US-0608810.
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-141592P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-634794/68.
N-PSDB; ABV72214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                   US6420521-B1
                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1999;
                                                                                 05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                     16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                   Protein
ABB78319
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Bishop PD;

Deisher TA,

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Uncleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate 2SIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar, nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The 2SIG33 and in assays to identify modulators of SIG33 expression and activity. The anti-2SIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-2SIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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                                                                                  The invention relates to zsig33-like peptides and their corresponding
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100.0%; Pred. No. 2.3e-101;
iive 0; Mismatches 0;
Disclosure; Page 27; 34pp; English.
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AAE23838 standard; Protein; 117 AA

AAE23838

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises ssig33-like peptides
                                                                                                                                                    Human; zsig33-like peptide; ZS33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33 protein.
                                                                                                                                                                                                                                                                                                                                          /note= "Human mature zsig33 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deisher TA,
                                                                                                                                                                                                                                                                                       1..23
/label- Signal_peptide
24..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 80-81; 89pp; English.
                                                                                                                                                                                                                                                                               Location/Qualifiers
                             AAE15883 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001; 2001WO-US15091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2000; 2000US-0569271.
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                          Human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-082982/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD25759
                                                                                                                                                                                                                                                                                                                                                                         WO200187933-A2
                                                                                                                                                                                                                                                  Homo saptens.
                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2001
                                                            AAE15883;
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RESULT 9
              AAE15883
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                                                                                                     DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                            Gaps
                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                  Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
                              Length 117;
                                                          Indels
                             Score 117; DB 23;
Pred. No. 2.3e-101;
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                                                         Mismatches
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100.0%;
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98WO-US22992.
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                                                          Conservative
                                         Best Local Similarity
Matches 117; Conserv
117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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29-OCT-1998;
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14-SEP-1998;
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07-OCT-1998;
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 Sequence
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                             Query Match
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteels. The PRO polypeptides are useful for detecting other PRO polypeptides, for inking bloactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating tresence of tumours. The polynucleotide sequences encoding the presence of tumours. The polynucleotide sequences encoding the presence of tumours. The polynucleotide sequences encoding pRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the human Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence cata for this patent was obtained in electronic sequence are sequenced by the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPSPGTVCSLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease; organ failure, atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; blosensor; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tumour.
                                          therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 117; DB 24; Length 117; 100.0%; Pred. No. 2.3e-101; Live 0; Mismatches 0; Indels 0;
                               New secreted and transmembrane PRO nucleic acids, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane, PRO, protein SEQ ID 442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; transmembrane protein; PRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU67066 standard; Protein; 117 AA
                                                                               Claim 12; Fig 442; 660pp; English.
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98WO-US12456.
98WO-US14552.
98WO-US17888.
98WO-US18824.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 117; Conservative
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     N-PSDB; ACA03823
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12-JUN-1998;
14-JUL-1998;
28-AUG-1998;
10-SEP-1998;
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001US-0872035.
2001US-0874503.
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2001US-0816744.
2001US-0828366.
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2001US-0854280.
2001US-0860216.
2001US-0866028.
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2001US-0886342.
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2001US-0908827.
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2001US-0796498.
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2000WO-US03565
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16-DEC-1999;
16-DEC-1999;
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98WO-US19094.
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09-JUL-2001;
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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                        2001US-0828366.
2001US-0854208.
2001US-0854280.
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2001US-0808689.
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Gerritsen ME, Goddard A,
                                                                                                                                                                                                                                                                                     aging, AIDS, or cancer
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       28-FEB-2001
09-MAR-2001
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3 Gao Sequence

100.0%; Score 117; DB 24; Length 117; 100.0%; Pred. No. 2.3e-101; Query Match Best Local Similarity 9

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02-DEC-1999; 99WO-US28564.
02-DEC-1999; 99WO-US28565.
16-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US3099.
22-DEC-1999; 99WO-US3099.
23-DEC-1999; 99WO-US30210.
05-JAN-2000; 200WO-US002119.
18-FEB-2000; 200WO-US00376.
11-FEB-2000; 200WO-US00376.
11-FEB-2000; 200WO-US00376.
11-FEB-2000; 200WO-US00319.
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2001US-0872035.
2001US-0874503.
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2001US-0887879.
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Smith V, Stewa
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22-MAR-2001; 2
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19-DEC-2001;
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    Mismatches
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98WO-US12456.
98WO-US17888.
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99WO-US28551
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    Matches 117; Conservative
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08-MAR-1999;
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(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

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-FEB-1
 The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in coll paractive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardlac insufficiency disorders. PRO156, and PRO186 critical capillary endothelial growth, and PRO136, PRO943, PRO828, PRO826, PRO8186, PRO943, PRO828, PRO826, PRO8186, PRO943, PRO828, PRO826, PRO1387 induce c-fos in endothelial growth, and are thus useful for treating cancerous tumours. PRO812 inhibits vascular conductedial growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of colls and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulated proliferation of cells and is thus useful for inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1314 and PRO1312 inhibiting tumour growth in cells in inhibiting tumour growth in the process survival proliferation of and PRO1312 is also enhances survival of cells induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with dermaticial, herpetiformis or coher computations associated with dermaticial, herpetiformis or crohm's cells and pro1312, PRO1322 and PRO1387 induce the proliferation and/or readifferentiation of chondrocytes in culture and cell function such as berger disease or other cells and the such in far such in the such in the useful for treating of chondrocytes in culture and cell such as provers in culture and server the and the such in the such 
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                                               Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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                                                                                                                                    Claim 12; Fig 442; 659pp; English.
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nes 117; Conservative
WPI; 2003-148238/14.
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              N-PSDB; ABX89361
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dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
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97US-049787P.
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97US-065186P.
97US-065311P.
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98US-088025P-
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98WO-US19437.
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16-SEP-1998;
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                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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     8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in inking a bloadrive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus compared in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus stimulate adrenal cortical capillary endothelial growth, and PRO136, PRO943, PRO943, PRO926, PRO943, PRO926, PRO943, PRO926, PRO1367 induce c-fos in endothelial growth, and PRO136, useful for treating cancerous tumours. PRO912 inhibits vascular cuseful for treating cancerous tumours. PRO912 inhibits vascular condothelial growth factor (VEGE) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in commands which would be beneficial in inhibiting tumour growth. PRO926, PRO1066, PRO1968, PRO1968, PRO1969, PRO1066, PRO1969, PRO1066, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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Wood WI;
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Berrara N, Rong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                             decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.
                                                                                                                                                                                                                                                                                                                     1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
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100.0%; Score 117; DB 24;
Best Local Similarity 100.0%; Pred. No. 2.3e-101;
Matches 117; Conservative 0; Mismatches 0;
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PR 24-JUN-1998; 98US-090646P
PR 24-JUN-1998; 98US-090644P
PR 25-JUN-1998; 98US-090644P
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PR 02-JUL-1998; 98US-091643P
PR 03-JUL-1998; 98US-091643P
PR 04-MUG-1998; 98US-091643P
PR 17-MUG-1998; 98US-09163P
PR 18-MUG-1998; 98US-09163P
PR 18-MUG-1998; 98US-09163P
PR 26-MUG-1998; 98US-091741P
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2000WO-US08439.
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20 - MAR - 2000; 30 - MAR - 2000; 31 - MAY - 2000; 32 - MAY - 2000; 32 - MAY - 2000; 32 - MAY - 2000; 33 - MAY - 2000; 34 - MAY - 2000; 35 - MAY - 2000; 36 - MAY - 1997; 36 - MAR - 1998; 36 - M
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                                                                                                                                                                                                              Human; PRO; hypertrophy of neonatal heart; anglogenesis; wound healing
                                                                                                                                        MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
                                                                                                               Gaps
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                                                                               ; Score 117; DB 24;
; Pred. No. 2.3e-101;
0; Mismatches 0;
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100.0%;
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                                                                               Query Match
Best Local Similarity 100.0
Matches 117; Conservative
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
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01-DEC-1999;
16-DEC-1999;
20-DEC-1999;
05-JAN-2000;
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              17-SEP-1998;
22-DEC-1998;
12-MAR-1999;
23-JUN-1999;
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-SEP-1998;
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 16-SEP-1998
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30-NOV-1999
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Search completed: September 11, 2003, 17:51:53 Job time : 123.257 secs

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Run on:

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
           US-09-989-735-268
US-09-990-444-268
US-09-991-181-268
US-09-980-730-268
US-09-989-734-268
US-09-999-734-268
US-09-993-693-268
US-09-993-693-268
US-09-993-673-268
US-09-993-673-268
                                                                                                                                                                        US-09-997-666-268
US-09-990-438-268
US-09-990-711-268
US-09-989-726-268
US-09-998-726-268
US-09-998-726-268
US-09-998-726-268
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US-09-997-683-268
US-09-989-729A-268
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US-09-997-601-268
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US-09-997-573-268
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STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sheppard, Paul O.
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09794987 Patent No. US20010041791A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA ZIP: 98102 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle STATE: WA
US-09-794-987-2
 Sequence 2, Appli
Sequence 26, Appl
Sequence 268, App
                                                                                                                              (without alignments)
237.266 Million cell updates/sec
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Sequence 268,
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                                                                                                           September 11, 2003, 17:55:57; Search time 71.9519 Seconds
                                                                                                                                                                                                      1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117
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(cgnz_6/ptodata/1/pubpaa/US07_buBCOMB.pep:*
(cgnz_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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(cgnz_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-853-253-2
US-09-989-722-268
US-09-989-722-268
US-09-989-727-268
US-09-989-737-268
US-09-989-731-268
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US-09-993-604-268
US-09-990-456-268
US-09-989-721-268
US-09-992-598-268
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                                                                                                                                                                                                                                                                                       541936 segs, 145912426 residues
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Sequence:
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Result Š

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Godowski, Paul J.
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Pred. No. 7.5e-104;
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100.0%; Pred. No. 7.5e-104;
Live 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.5
Matches 117; Conservative 0; Mismatches
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APPLICANT: SHEPPARD, PAUL
APPLICANT: DEISHER, THERESA
APPLICANT: DEISHER, THERESA
APPLICANT: DEISHER, PAUL
TITLE OF INVENTION: 281933-11ke Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEO ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09853253 Patent No. US20020055156A1
LENGTH: 117 amino acids
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: JASPERS, STEPHEN
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Best Local Similarity 100.C
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US-09-853-253-2
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APPLICANT:
APPLICANT:
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APPLICANT GUITES, ALALIA L.
APPLICANT GUITES, ALALIA L.
APPLICANT GUITES, ALALIA L.
APPLICANT GUITES, ALALIA L.
APPLICANT SUL SIDERAL CALL SECONDARY A.
APPLICANT SULPHILATOR TO STATE A.
APPLICANT SULPHILATOR TO STATE A.
APPLICANT TOWNS, ALALIA ELCOLIA F.
APPLICANT SULPHILATOR SULPHILA CALL SECONDARY A.
APPLICANT TOWNS, ALALIA ELCOLIA F.
APPLICANT TOWNS, ALALIA ELCOLIA G.
APPLICANT TOWNS, ALALIA ELCOLIA G.
APPLICANT SULPHILATOR SULPHILA CALL SECONDARY TOWNS, ALALIA ELCOLIA G.
APPLICANT SULPHILATOR SULPHILA CALL SECONDARY TOWNS, ALEXA CALL SECONDARY TOWNS, ALEXA CALL SULPHILA CALL SULP
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DR APPLICATION NUMBER: 60/08810

PR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/08824

PR APLICATION NUMBER: 60/08826

PR APPLICATION NUMBER: 60/08826

PR FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                             NA APPLICATION NUMBER: 60/088658

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088076

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-12

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089514

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-19
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10
                                                  APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
PPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
PPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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100.0%; Pred. No. 7.5e-104
ive 0; Mismatches 0;
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091633
DR FILING DATE: 1998-07-02
DR APLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/092182
DR FILING DATE: 1998-07-09
                                                                     R APPLICATION NUMBER: 60/090542

R FILING DATE: 1998-66-24

R APPLICATION NUMBER: 60/090557

R APPLICATION NUMBER: 60/090567

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R APPLICATION NUMBER: 60/090863

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R APPLICATION NUMBER: 60/091360

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091408

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01
    APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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Best Local Similarity 100.
Matches 117; Conservative
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61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE Gaps g ò QQ ò

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> Sequence 268, Application US/09989723 Patent No. US20020072092A1 GENERAL INFORMATION: Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. Baker, Kevin P. Botstein, David US-09-989-723-268 APPLICANT: APPLICANT: APPLICANT:

Gerritsen, Mary E. Fong, Sherman Gerber, Hanspeter Goddard, Audrey APPLICANT:
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APPLICANT:

Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L.

DR APPLICATION NUMBER: 60/088742

R FILING DATE: 1998-06-10

R RILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088810

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088826

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R RILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088658

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/08861

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088816

FILING DATE: 1998-06-10

DR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/089514
DR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/089532
DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089538
DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089598
DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089598
DR FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 PAPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16

[LING DATE: 1998-06-1]

APPLICATION NUMBER: 60/089512

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APPLICANT: ROY, Margaret Ann APPLICANT: ROY, Margaret Ann APPLICANT: Stewart Timothy A. APPLICANT: Stewart Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Walliams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I. APPLICANT: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLG2
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 1997-16-16
PRIOR APPLICATION NUMBER: 60/062260
PRIOR APPLICATION NUMBER: 60/062260
PRIOR APPLICATION NUMBER: 60/065186
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APPLICATION UNMBER: 60/066770
PILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
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FILING DATE: 1998-03-20
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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NG DATE: 1998-06-05
ICATION NUMBER: 60/088217
NG DATE: 1998-06-05
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FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
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1998-06-03
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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1998-06-04
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FILING DATE: 1998-06-09
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FILING DATE: 1998-06-10
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Kljavin, Ivar J.
                          Napier, Mary A.
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R APPLICATION NUMBER: 60/089653
RR FILING DATE: 1998-06-17
RR APPLICATION NUMBER: 60/089801
RFILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089918
R FILING DATE: 1998-06-18

R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-19
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
R APPLICATION NUMBER: 60/090252
R RILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-23

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R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-66-24

R APPLICATION NUMBER: 60/090431

R APPLICATION NUMBER: 60/090435

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R APPLICATION NUMBER: 60/090444

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090455

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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24

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APPLICATING DATE INVOICED CONTINUED TO THE REPORT OF THE R
                                                                            Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                         Roy, Margaret Ann
Stewart, Timothy A
Paoni, Nicholas F
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APPLICANT:
                                                                      APPLICANT APPLICANT
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        PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PELING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-06-26
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PRIOR FILING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PAPPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1938-07-01
PRIOR PLING DATE: 1938-07-02
PRIOR PAPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1938-07-02
PRIOR FILING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091635
PRIOR APPLICATION NUMBER: 60/091636
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Gerber, Hanspeter
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Napier, Mary A.
Pan, James
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PRIOR PELICATION NUMBER: 60/08824
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PRIOR PELICATION NUMBER: 60/08921
PRIOR PELICATION NUMBER: 60/08929
PRIOR PELICATION NUMBER: 60/08923
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PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978 Sequence 268, Application US/09989727 Patent No. US20020072497A1 GENERAL INFORMATION: Godowski, Paul J. Grimaldi, J. Christopher APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey Gurney, Austin L. Ouery Match Best Local Similarity 100.0 Matches 117; Conservative US-09-989-727-268 APPLICANT: APPLICANT: APPLICANT q ò á

Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A.

> APPLICANT: APPLICANT: APPLICANT:

Kljavin,Ivar J. Napier,Mary A.

APPLICANT: APPLICANT:

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R APPLICATION NUMBER: 60/08861

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/08895

R APLICATION NUMBER: 60/089105

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-12

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

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R FILING DATE: 1998-06-17
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R RETLING DATE: 1998-06-18

R FILING DATE: 1998-06-19

R FILING DATE: 1998-06-19

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089948

R APPLICATION NUMBER: 60/089952

R FILING DATE: 1998-06-19

R FILING DATE: 1998-06-22

R FILING DATE: 1998-06-23

R FILING DATE: 1998-06-23

R FILING DATE: 1998-06-23

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090435

R APPLICATION NUMBER: 60/090444

R APPLICATION NUMBER: 60/090444

R APPLICATION NUMBER: 60/090445

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/09045

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090535

R APPLICATION NUMBER: 60/090535
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-25
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FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
                              ION NUMBER: 60/088826
ATE: 1998-06-10
                                                                                                APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11
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                 APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: William I.
APPLICANT: William I.
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PRIOR APPLICATION NUMBER: 05/049787
PRIOR PLING DATE: 1997-06-16
PRIOR PLING DATE: 1997-06-16
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-24
PRIOR PLING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998 -0.3.20
PRIOR FILING DATE: 1998 -0.3.20
PRIOR FILING DATE: 1998 -0.3.20
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998 -0.5.28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PELING DATE: 1998 -0.6.02
PRIOR PELING DATE: 1998 -0.6.02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/087827
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PILING DATE: 1998 -0.6.04
PRIOR PILING DATE: 1998 -0.6.04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PILING DATE: 1998 -0.6.04
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DR FILING DATE: 1998-06-04

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088029

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088030

DR APPLICATION NUMBER: 60/088033

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088025

DR FILING DATE: 1998-06-04

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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-05
R PILING DATE: 1998-06-05
R PILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088658
R FILING DATE: 1998-06-09
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Tumas, Daniel
APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmëmbrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
                                                                                                                                CURREMY APPLICATION NUMBER: US/09/989,731
CURREMY FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06311
PRIOR PELICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELICATION NUMBER: 60/065311
PRIOR PELICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR PELICATION NUMBER: 60/08322
PRIOR FILING DATE: 1998-03-20
PRIOR PELICATION NUMBER: 60/08709
PRIOR FILING DATE: 1998-06-22
PRIOR PELICATION NUMBER: 60/08709
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PRIOR PELING DATE: 1998-06-02
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Best Local Similarity 100.0%; Pred. No. 7.5e-104;
Matches 117; Conservative 0; Mismatches 0;
                                         PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09063
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091638
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091638
PRIOR APPLICATION NUMBER: 60/091638
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091638
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Gerber, Hanspeter
Gertisen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-07-07
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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                             FILING DATE: 1998-06-25
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PRIOR APPLICATION WUNBER: 60/08861

PRIOR PLICATION WUNBER: 60/08861

PRIOR PLICATION WUNBER: 60/08861

PRIOR PLICATION WUNBER: 60/08861

PRIOR PLICATION WUNBER: 60/08865

PRIOR PLICATION WUNBER: 60/08876

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PRIOR PLICATION WUNBER: 60/08874

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PRIOR PLICATION WUNBER: 60/08873

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PRIOR PLICATION WUNBER: 60/09973

PRIOR PRIOR PLICATION WUNBER: 60/09973

PRIOR PRIOR PLICATION WUNBER: 60
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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100.0%; Pred. No. 7.5e-104;
Live 0; Mismatches 0;
                                                                                     R APPLICATION NUMBER: 60/090696
R APPLICATION NUMBER: 60/090696
R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                         R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R APPLICATION NUMBER: 60/091626
R APPLICATION NUMBER: 60/091638
R APPLICATION NUMBER: 60/091638
R FILING DATE: 1998-07-02
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R APPLICATION NUMBER: 60/091978
R PELLING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R RELLING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R FILING DATE: 1998-07-07
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Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/091478
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary'E.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Napier, Mary A.
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Best Local Similarity 100.
Matches 117; Conservative
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NR FILING DATE: 1997-06-16

NR APPLICATION NUMBER: 60/062250

NR FILING DATE: 1997-10-17

NR APPLICATION NUMBER: 60/065186

NR FILING DATE: 1997-11-12

NR APPLICATION NUMBER: 60/065311

NR FILING DATE: 1997-11-13

NR FILING DATE: 1997-11-24

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NR FILING DATE: 1997-11-24
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R APPLICATION NUMBER: 60/088026
R APPLICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-07
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R APPLICATION NUMBER: 60/088028
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R APPLICATION NUMBER: 60/088167

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R APPLICATION NUMBER: 60/088212
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R FILING DATE: 1998-06-11
R APPLICATION NUMBER; 60/088861
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R APPLICATION NUMBER: 60/084600

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R APPLICATION NUMBER: 60/087106

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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088021
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Actids Encoding the Same
FILE REFERENCE: P2730PIC15
CURRENT APPLICATION NUMBER: US/09/991,073
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; Pred. No. 7.5e-104;
0; Mismatches 0;
                  PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR APPLICATION NUMBER: 60/090862
PRIOR PILING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09154
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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Patent No. US20020127576A1
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
     APPLICATION NUMBER: 60/090696
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 100.0
Matches 117; Conservative
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APPLICANT: Ashkenazi, Avi J.
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR PPLICATION NUMBER: 60/089514
PRIOR PILING DATE: 1998-06-17
PRIOR PPLICATION NUMBER: 60/089532
PRIOR PILING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PILING DATE: 1998-06-17
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PRIOR PLING DATE: 1998-06-17
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RR FILING DATE: 1998-06-19

RR FILING DATE: 1998-06-22

RR APPLICATION NUMBER: 60/090252

RR APPLICATION NUMBER: 60/090254

RR FILING DATE: 1998-06-22

RR FILING DATE: 1998-06-22

RR FILING DATE: 1998-06-23

RR FILING DATE: 1998-06-23

RR APPLICATION NUMBER: 60/090439

RR FILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090439

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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090696
1998-06-
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR FILICA DATE: 2001-11-14
PRIOR RILICATION NUMBER: 60/049787

Watanabe, Colin K. Williams, P. Mickey Wood, William I.

APPLICANT: APPLICANT:

APPLICANT

Roy, Margaret Ann Stewart, Timothy A.

APPLICANT: APPLICANT:

Tumas, Daniel

Paoni, Nicholas F.

Napier, Mary A. Pan, James

Godowski, Paul J. Grimaldi, J. Christopher

Gurney, Austin L.

Kljavin, Ivar J.

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT

APPLICANT APPLICANT

Gerritsen, Mary E. Goddard, Audrey Fong, Sherman Gerber, Hanspeter

APPLICANT: APPLICANT:

APPLICANT

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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/09154
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PRIOR APPLICATION NUMBER: 60/09159
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/09182
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Best Local Similarity 100.
Matches 117; Conservative
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APPLICANT: Ashkenazi, Avi J.
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Eaton, Dan L.
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NUMBER: 60/06/250 1997-10-17	NUMBER: 60/065186	: 1997-11-12 NUMBER: 60/065311	1997-11-13 NUMBER: 60/066770	1997-11-24	NUMBER: 60/075945 1998-02-25		TUMBE	1998-04-28 NUMBER: 60/084600	1998-05-07 NIIMBER: 60.087106	NUMBER: 00/08/100 1998-05-28	NUMBER: 60/087607	1998-08-02 NUMBER: 60/087609	1998-06-02 NUMBER: 60/087759	1998-06-02	N NUMBER: 60/087827 E: 1998-06-03	NUMBER: 60/088021	1998-06-04 NIMBER: 60/088025	1998-06-04	NUMBER: 60/088026 : 1998-06-04	NUMBER: 60/088028	1998-06-04 NIMBER: 60/088029	1998-06	NUMBER: 60/088030 1998-06-04	NUMBER: 60/088033	1998-06-04 NUMBER: 60/088326	1998-06-04	NUMBER: 60/088167 1998-06-05	N NUMBER: 60/088202	NUMBER: 60/088212	1998-06-05 NUMBER: 60/088217	1998-06-05	1998-06-09	NUMBER: 60/088734 1998-06-10	NUMBER: 60/088738	1998-08-10 NUMBER: 60/088742	1998-06-10	9	NUMBER: 60/088824 1998-06-10	NUMBER: 60/088826	1998-06-10 NUMBER: 60/088858	90	NUMBER: 60/088861 1998-06-11	R: 60	1998-05-11 NUMBER: 60/089105	: 1998-06-12 NUMBER: 60/089440
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Gurney, Austin L.
Kljavin,Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Eaton, Dan L.
Ferrara, Napoleone
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Paoni, Nicholas F.
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Gerber, Hanspeter
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Matches 117; Conservative
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ö 1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60 61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117 APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C25 ; 0 Length 117; Indels Query Match 100.0%; Score 117; DB 10; Best Local Similarity 100.0%; Pred. No. 7.5e-104; Matches 117; Conservative 0; Mismatches 0; CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/993,604
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PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 Sequence 268, Application US/09993604 Patent No. US20020137075A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. Godowski, Paul J. Grimaldi, J. Christopher Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Ferrara, Napoleone Pan, James Paoni, Nicholas F. Gurney, Austin L. Kljavin, Ivar J. Baker, Kevin P. Botstein, David Napier, Mary A. Eaton, Dan L. -09-993-604-268 APPLICANT:
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088861
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27309102.
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
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100.0%; Pred. No. 7.5e-104;
Live 0; Mismatches 0;
               PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
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APPLICATION NUMBER: 60/091544
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
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Matches 117; Conservative
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Botstein, David
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R FILING DATE: 1998-66-23
R PAPLICATION NUMBER: 60/090429
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R FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-26
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091519
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CURRENT FILIG DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
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PRIOR FILING DATE: 1997-11-24
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; Patent No. US20020142961A1

; GENERAL INFORMATION:

APPLICANT: AShkenazi, avi J.
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Napier,Mary A.
Pan,James
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Gerber, Hanspeter
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Botstein, David
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Godowski, Paul
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A APPLICATION NUMBER: 60/088033
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A APPLICATION NUMBER: 60/088326
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R APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/088021
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  FILING DATE: 1998-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C20
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                                                                                                                                                                                                                             Length 117;
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PRIOR PILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065260
PRIOR FILING DATE: 1997-11-12
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PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/056570
               PRIOR FILING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 268, Application US/09992598 Patent No. US20020150384A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
APPLICATION NUMBER: 60/091633
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FILING DATE: 1998-03-20
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Napier, Mary A.
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Botstein, David
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US-09-992-598-268
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PRIOR APPLICATION NUMBER: 60/09024
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PRIOR APPLICATION NUMBER: 60/09035
PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/09035
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PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09035
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PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090154
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090154
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090159
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-07-02
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 11, 2003, 17:46:37; Search time 44.4225 Seconds (without alignments) 253.289 Million cell updates/sec Run on:

US-09-853-253-2 117 1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283308 seqs, 96168682 residues Searched:

0 Word size :

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qhrelin precursor			hypothetical prote	transcription requ	hypothetical prote	~	hypothetical prote			Ω	DNA-directed DNA p	probable ABC-trans	hypothetical prote	prolyl-tRNA synthe	multidrug resistan	spliceosome-associ	amidophosphoribosy	activin receptor-1	serine/threonine k	hypothetical prote	hypothetical prote	probable 0-antigen	atp synthase beta	conserved hypothet	hypothetical prote	sensor protein tor	sensor protein tor	protein-histidine
SUMMARIES	OI S	A59316					: T04453	2 PH1333							A86195			2 A47655			3C2491				: D90541		H9752	D9077	н8563	G64840
	Query Match Length DB				302			22										464			205								~	904
dР	Query	100.0	15.4	6.8			6.8		•	•	٠	•	٠		٠	٠		6.0	٠		0.9	•	0.9			0.9		0.9	0.9	0.9
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B99316
ghrelin precursor - rat
ghrelin species: Rattus norvegicus (Norway rat)
C; pecies: Rattus norvegicus (Norway rat)
C; bate: 16-Jun-2000 #sequence_revision 16-Jun-2000
C; bate: 16-Jun-2000 #sequence_revision 16-Jun-2000
R; Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A; Theference number: A59316; MUID:20067959; PMID:10604470
A; Reference number: A59316
A; Status: not compared with conceptual translation

RESULT 2

aconitate hydratas BOLFI protein - hu myoblast city prot hypothetical prote hypothetical prote hypothetical prote cold-shock domain troponin T, cardia pancreatic hormone hypothetical prote conserved hypothet hypothetical prote conserved hypothet hypothetical prote hypothetical prote pyothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	S-2000 #text_change 21-Jul-2000 M.; Matsuo, H.; Kangawa, K. g acylated peptide from stomach. ID:10604470 ation ; PIDN:BAA89371.1; PID:96691572 ne calls imulates the release of somatotropin (gr ted <sig> #status predicted <ctp> #status predicted <ctp> #status experimental DB 1; Length 117;</ctp></ctp></sig>	<pre>imflarity 100.0%; Pred. No. 3.2e-109; conservative 0; Mismatches 0; Indels 0; Gaps 0; preservative 0; Mismatches 0; Indels 0; Gaps 0; preservative 0; Mismatches 0; Indels 0; preservative 0; Indels 0; preservative 0; Indels 0; preservative 0; preserv</pre>
B83451 00BEL0 1003E10 515010 (83241 697241 687574 848790 PH3402 E83141 F82266 A71193 AF2124	ALIGNMENT sion 16-Jun ; Nakazato, ne-releasin 0067959; PM tual transl 1099 stomach endocri 11999 stomach et stomach st s	; Pred. No. 3 0, Mismatche DLAMAGSSFLSPEH DLAMAGSSFLSPEH PLUIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
0100000000000000	lin hor onc onc 34; 7 t 7 t 6 t 6 t 6 t 6 t 7 t 7 t 7 t 7 t 7 t 7 t 8	LEEL FNA FNA FNA
910 1939 1165 52 52 659 669 80 1104 1104	human preproghrelin lens (man) #sequence_revis ta, 1999 A growth-hormor A 59316; MUID:20 A 59316; MUID:20 GB:AB029434; NI ce: tissue stomm CG:AB029434; NI ce: tissue stomm A growth-hormor A	.Larity 100.0%; Conservative PGTVCSLLLGMIWLD IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
00000	phenilen s, 1 s, 1 secce: secce: s	nse nse TVC EGA
<i>.</i>	2	SPG' SPG' SPG' SPG' SPG' SPG' SPG'
~~~~ <u>@</u>	SULT 1 9316 Trelin precursor - human Alternate names: preproghrelin Species: Homo saplens (man) Date: 16-Jun-2000 #sequence_revi, ture 402, 656-660, 1999 Title: Ghrelin is a growth-hormo Reference number: A59316 Accession: A59316 Accession: A59316 Accession: A59316 Accession: A59316 Conserved to Compared with concep Molecule type: mRNA Residues: 1-117 <koj> Cross-references: GB-AB029434; N Residues: 1-117 <koj> Cross-references: GB-AB029434; N Cross-references: GB-AB029434; N Experimental source: tissue stom Note: submitted to GenBank, June Comment: Ghrelin secreted by the Superfamily: motilin Keywords: hormone; lipoprotein; 1-23/Domain: signal sequence #st. 24-51/Product: ghrelin #status p 52-117/Domain: carboxyl-terminal 26/Binding site: octanoate (Ser) Ouery Match</koj></koj>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1 A59316 Mirelin precursor - hum N:Alternate names: prepp. C;Species: Homo sapiens C;Accession: A59316 R;KOjima, M.; Hosoda, H Nature 402, 656-660, 19 A;Title: Ghrelin is a g A;Reference number: A59316 A;Title: Ghrelin is a g A;Reference number: A59316 A;Accession: A59316 A;Actaus: not compared A;Molecule type: mRNA A;Residues: 1-117 <koj>A;Cross-references: GB:,A;Experimental source: C;Comment: Ghrelin secric;Superfamily: motilin F;1-23/Domain: signal s;F;24-51/Product: ghrelin serric;Superfamily: motilin F;1-24/Domain: signal s;F;26/Binding site: octan</koj>	Best Local Matches 1: Qy Db Qy 60

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transcription regulator LysR family homolog SnpR - Streptomyces lividans C;Species: Streptomyces lividans C;Species: Streptomyces lividans C;Date: 1990 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000 C;Accession: A48890 R:Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T. Can. J. Microblol. 38, 912-920, 1992 A;Tile: Cloning of genetic loci involved in endoprotease activity in Streptomyces 11 A;Reference number: A48990; MUID:93099553; PMID:1464066
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH133
R;Wasserman, R.; Gallli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor ly A;Reference number: PH1302; MUID:93094761; PMID:1460419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C'Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 30-Apr.1999 #sequence_revision 30-Apr.1999 #text_change 30-Apr.1999
C;Accession: T04453
R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998
A;Reference number: 215360
A;Reference number: 215360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Accession: A48990
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-344 <BUT>
A/Residues: 1-344 <BUT>
A/Residues: Sequence extracted from NCBI backbone (NCBIN:121210, NCBIP:121213)
C/Superfamily: Pseudomonas putida regulatory protein catR
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A;Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1;
A;Note: F4D11.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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A Residues: 1-483 <BEV>
A: Cross-references: EMBL:AL022537
A: Experimental source: cultivar Columbia; BAC clone F4D11
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100.0%; Pred. No. 6.2;
tive 0; Mismatches
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A; Molecule type: DNA
A; Residues: 1-22 <WAST
C; Keywords: heterotetramer; immunoglobulin
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       99 RALAGWLR 106
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Contents: 66
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                                                                                                                  RESULT
A48990
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                                                            A/Cross-references: GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g6691570
A/Experimental source: strain SD: tissue stomach endocrine cells
A/Note: submitted to GenBank, June 1999
C/Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growt c/Superfamily: motilin
C/Reywords: hormone; lipoprotein; stomach
E/1-23/Domain: signal sequence #status predicted <SIG>
E/24-51/Product: ghrelin #status predicted <MAT>
E/52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
E/26/Binding site: octanoate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A49221
R; Naturo, J.P.; Yikang, D.; Giron, J.A.; Savarino, S.J.; Kothary, M.H.; Hall, R.
Infect. Immun. 61, 1126-1131, 1993
A; Title: Aggregative adherence fimbria I expression in enteroaggregative Escherichia col
A; Reference number: A49221; MUID: 93162805; PMID: 8094379
A; Contents: 17-2, serotype 03: H2
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C;Accession: A49221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14K aggregative adherence fimbriae I protein - Escherichia coli (fragment) C; Species: Escherichia coli
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100.0%; Pred. No. 4.2;
tive 0; Mismatches 0; Indels
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A)Accession: A4921
A)Accession: preliminary
A)Acciscule type: protein
A)Residues: 1-23 AANATA
A)Note: sequence extracted from NCBI backbone (NCBIP:125179)
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100.0%; Pred. No. 0.5;
Live 0; Mismatches
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A; Molecule type: mRNA; protein A; Residues: 1-117 <KOJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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A;Cross-references: GB:AE001938; GB:AE000513; NID:g6458553; PIDN:AAF10422.1; PID:g645
A;Experimental source: strain Rl
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: F81201
R; Heidelberg, J.E.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A802035; MUID: 20406833; PMID: 10952301
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A.Experimental source: serogroup O1; strain N16961; blotype El Tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase III, epsilon chain VC2233 [imported] - Vibrio cholerae (strain N16961
                             Riwhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA;Reference number: A75250; MUID:20036896; PMID:10567266
A;Scatus: preliminary
A;Status: preliminary
A;Residues: 1-216 <WHI>
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100.0%; Pred. No. 32;
Live 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-247 <HEI
   C; Accession: B75469
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A; Map position: 1
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A;Gene: DR0838
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CyAccession: F83841
Nucleic Acids Res. 28, 4317-4311, 2000
A;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Accession: F83841
A;Accession: F83841
A;Accession: F83841
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-138 csTro>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05253.1; GSPDB:GNOCA: Experimental source: strain C-125
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A;Accession: B83523
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <STO>
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Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: B83523
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
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Experimental source: strain PA01
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B75469
B75469
C; Species: Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein BH1534 [imported] – Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                     0; Indels
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   Length 22;
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C;Superfamily: Bacillus subtilis hypothetical protein yndB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 7; DB 2;
100.0%; Pred. No. 22;
tive 0; Mismatches
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6.0%; Score 7; DB 2;
100.0%; Pred. No. 4.8;
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100.0%; Pred. No. 31;
ative 0; Mismatches
                                                                     0; Mismatches
                                    100.08;
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 7; Conservative
                                                                     Conservative
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MPSPGTV 90
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10 EVRFNAP 16
                                                                                                                                           7 VCSLLLL 13
                                                                                                                                                                                VCSLLLL 12
                                 Best Local Similarity
Matches 7; Conserv
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   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics
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123 GSSFLSP 129
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   C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable ABC-transporter inner membrane protein SbmA sbmA [imported] - Salmonella enteria probable ABC-transporter inner membrane protein SbmA sbmA [imported] - Salmonella enterica subsp. enterica serovar Typhi A; Note: this spooles has also been called Salmonella typhi c; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: AGG548 R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nathers: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Accession: AGG548 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-406 cPAR> A; Residues: 1-406 cPAR> A; Residues: 1-406 cPAR> A; Cross-references: GB:AL513382; PIDN:CAD08831.1; PID:g16501645; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C. Species: Arabidopsis thaliana (mouse-ear cress) (C. Species: Arabidopsis thaliana (mouse-ear cress) (C. Species: Och Mar. 2001 #sequence_revision 02-mar-2001 #text_change 31-mar-2001 (C. Accession: A86195 (C. Accession: A86195 (C. Accession: A86195 (C. A. Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C. Hughes, B.; Huizar, L. Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Naturer, N.F.; Hughes, B.; Huizar, L. Naturer, J.L.; J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Rowley, D.; Sakano, H. A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A. Reference number: A86141; MUID: 21016719; PMID: 11130712
                                       A;Cross-references: GB:U32699; GB:L42023; NID:g3212180; PIDN:AAC21808.1; PID:g1573090; C;Genetics:
                                                                                                                   A;Gene: dnaQ
A;Cene: dnaQ
A;Pathway: DNA biosynthesis
C;Superfamily: dnaQ protein
C;Keywords: DNA biosynthesis; DNA replication initiation; nucleotidyltransferase
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A;Cross-references: GB:AE005172; NID:g8810462; PIDN:AAF80123.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                  Query Match 6.0%; Score 7; DB 2; Length 256; Best Local Similarity 100.0%; Pred. No. 36; Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 53;
tive 0; Mismatches 0; Indels
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 VGIKLSG 267
                             A; Residues: 1-256 <TIGR>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-435 <STO>
A; Molecule type: DNA
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A;Gene: sbmA
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projivitera synthetase [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C; Accession: F87488
R; Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Nutl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Titlo: Complete Ganome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-443 <STO>
A;Cross-references: GB:AE005673; NID:g13423386; PIDN:AAK23906.1; GSPDB:GN00148
                                                                                   Length 435;
                                                                                                                                                  0; Indels
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. 57;
                                                                                         DB 2;
                                                                                                                    56;
                                                                                   6.0%; Score 7; DB 2
100.0%; Pred. No. 56;
vative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches
A;Map position: 1
C;Superfamily: flavonol O3-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: September 11, 2003, 17:57:03 Job time: 47.4225 secs
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C;Superfamily: proline-tRNA ligase proS
                                                        Ouery Match
Best Local Similarity الاس.
من 7; Conservative
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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 11, 2003, 17:30:37 ; Search time 22.5241 Seconds
(without alignments)
244.278 Million cell updates/sec

US-09-853-253-2 117 1 MPSPGTVCSLLLLGMLMLDL......LGKFLQDILWEEAKEAPADK 117 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_41:* Database :

STIMMARTES

		Description	Q9ubu3 homo sapien	canis	_		Q9bd16 bos taurus	Q9gky5 sus scrofa	Q91127 streptomyce			P43745 haemophilus			Q15428 homo sapien	ม เมาร	Q55038 synechococc	O00238 homo sapien	-	P58356 escherichia	P39453 escherichia		epste			_	P02783 rattus norv	homo	Q16568 homo sapien	proto				Q8eh77 shewanella	P56388 mus musculu
SUMMARIES		ar T	Σ	GHRL_CANFA	GHRL_MOUSE	GHRL_RAT	GHRL_BOVIN	GHRL_PIG	MPR2_STRCO	MPRR_STRLI	DP3E_PASMU	DP3E_HAEIN	CHM1_BRARE	NAS1_HORVU	S3A2_HUMAN	S3A2_MOUSE	PUR1_SYNP7	BMRB_HUMAN	BMRB_MOUSE	TORS_ECO57	TORS_ECOLI	SPK_HUMAN	V120_EBV	PAHO_CHICK	RL36_TRIHM	RBFA_MYCPU	SVS4_RAT	SY27_HUMAN	CART_HUMAN	NU3M_PROWI	MSP1_GLORO	MSP2_GLORO	MSP3_GLORO	ACPS_SHEON	CART_MOUSE
		Length DB	117 1	117 1	117 1	117 1	116 1	118 1	328 1	344 1	253 1							502 1					1239 1	80 1	105 1	112 1	112 1	112 1	116 1	117 1	125 1	125 1	125 1	127 1	129 1
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	Result	No. Score	1 11	2 1	3	4	5	9	7	<b>&amp;</b>	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

P49192 rattus norv 006655 macropus eu P0411 homo sapien P4911 monodelphis 09hmn2 halobacteri P08904 bos taurus 070300 mus musculu P43343 serratia ma P25663 escherichia P17314 triticum ae P03927 xenopus lae P21760 gallus gall
CART_RAT LCA_MACEU CSF2_HUMAN TTHY_MONDO PFDA_HALNI RNS6_BOVIN PSPN_MOUSE MUG_SERMA SSPB_ECOLI IA03_WHEAT NUGM_XENLA EFAB_CHICK
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129 144 144 154 154 162 162 163 178
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6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

ALIGNMENTS	RESULT 1 GHRL_HUMAN ID GHRL_HUMAN STANDARD; PRT; 117 AA.	AC Q9UBU3; Q8TAT9; Q9H3R3; DT 28-FEB-2003 (Rel. 41, Created)	DT 28-FEB-2003 (Rel. 41, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update)			Homo sapiens (Human).		NCBI_TaxID=9606;		RX MEDLINE-20067959; PubMed-10604470; RA Kolima M. Hosoda H. Date V. Nakazato M. Matsuo H. Kangawa K.	"Ghrelin is a growth-hormone-releasing acylated peptide from	RT stomach."; B1 Nature 400:656-660/1000)			KA NOJIMA M.; RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.		RP SEQUENCE FROM N.A. (ISOFORM 1).			RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.			RT "Genomic organization of the human Ghrelin gene.";				KX MEDLINE=2238825/; PubMed=124//932; RA Straushera R.I., Pelngold E.A., Grouse L.H., Derge J.G.,		RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Da Honking D.B. Tordan H. Morra T. May C.T. Wang T. Waleh B.			RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Mullahv S.J.,			KA VIIIalion D.K., Muzhy D.M., Sodergren E.J., Lu A., Glidbs K.A.,  KA VIIIalion D.K., Muzhy D.M., Sodergren E.J., Lu A., Glidbs K.A.,			KA Kodriguez A.C., Grimwood J., Schmutz J., Myers K.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
	a o H	4 D	ΔΔ	Δ.	ט ב	00	0 (	0 2	; ας	<b>24</b> 12	: 24	<b>C</b> C	: 14	CC (	<b>x x</b>	~	<u>α</u> α	i nci	~	04 D	4 24	<u>a</u>	<b>6</b> 4 6	* 24	<u>r</u>	<b>P</b> (	* *	`~	<u>α</u> ; Δ	<b>Ω</b>	<u>a</u>	<b>α</b> α	: ex	<b>6</b> 2. (	¥ 0	: 24	α; ι	* #	

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117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
   SEQUENCE
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GHRL_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
Isold=09043-1; Sequence=Displayed;
Name=2; Synonyms=del-Glni4-ghrelin;
Isold=090803-2; Sequence=VSP_003245;
FPM: O-n-octanoylation is essential for activity.
SIMILARITY: BELONGS TO THE WOTILIN FAMILY.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infoblogen.fr/services/chromcancer/Genes/GhrelinID327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
GO; GO:0007186; P:growth hormone receptor ligand activity; TAS.
GO; GO:0007186; P:groteln signaling; TAS.
GO; GO:0007186; P:groteln suppled receptor protein signalin. . .; TAS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_ghrelin.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                          Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                           MEDIINE-21203998; Pubmed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative spilcing.
                                                                                                                               Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHRELIN.
REMOVED IN MATURE FORM.
N-OCTANOATE.
Missing (in isoform 2).
/FTId-VSP_003245.
L -> M (IN REF. 5).
                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                 TISSUE-Stomach;
MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB035700; BAB19045.1; -. EMBL, AJ25278; CAB65733.1; -. EMBL, AF296558; AAG10300.1; -. EMBL; BC025791; AAH25791.1; -. PIR; A59316; A59316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB029434; BAA89371.1; -.
                                and mouse cDNA sequences.
                                                                                24-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                SEQUENCE OF
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PROPEP
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                                    ö
                                                                     -i- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

-i- SUBCELLULAR LOCATION: Secreted.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD332162; Preproghrelin; 1. Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghralin precursor (Growth hormone secretagogue) (Growth hormone
releasing peptide) (Motilin-related peptide).
GHRL OR MTMRP.
                                    ö
   Length 117;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fundus."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
IISSUE-Gastric fundus;
Tomasetto C., Wendling C., Rio M.-C., Poitras P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms-2;
                                    ö
100.0%; Score 117; DB 1;
100.0%; Pred. No. 8e-111;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-1; Synonyms-Ghrelin;
IsoId-Q9BEF8-1; Sequence-Displayed;
Name-2; Synonyms-del-Ginl4-ghrelin;
IsoId-Q9BEF8-2; Sequence-vSP_003244;
-!- PTM: O-n-octanoylation is essential for act-
-!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                     117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                              GHRL_CANFA STANDARD; F Q9BEF8; Q9BEF7; 28-FEB-2003 (Rel. 41, free controlled)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ298295; CAC29155.1; -. EMBL; AJ298296; CAC29156.1; -.
                                    Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
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PROPEP
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Kojima M., Hosoda H., Matsuo H., Kangawa K.; "Ghrelin: discovery of the natural endogenous ligand for the growth

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinoe; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                      GHRL_MOUSE STANDARD; PRT; 117 AA.
09E0XJ. 09WUZ1;
28-FED-2003 (Rel. 41, Created)
28-FED-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
66relin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motillin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
                                                                                                DB 1; Length 117;
                                                                                                  Db 1,
. 6.3e-11;
. . 0; Indels
N-OCTANOATE (BY SIMILARITY).
Missing (in isoform 2).
/FTId-VSP_003244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse mRNA for preproghrelin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                        3E57FED9D1847CF7 CRC64;
                                                                                                                                   0; Mismatches
                                                                                                                  Pred. No.
                                                                                                Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Stomach;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Stomach;
MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21203998; PubMed-11306336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                       36 QQRKESKKPPAKLQPRAL 53
                                                                                                                                                                                             QORKESKKPPAKLQPRAL 53
                                                        13007 MW;
                                                                                            15.4%;
                                                                                                                Local Similarity 100.
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                      117 AA;
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kojima M.
                  VARSPLIC
                                                                                              Query Match
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                                                                                                                                                                                                                                                                                          GHRL_MOUSE
                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                      RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                             Name=1; Synonyms-Ghrelin; Name=1; Synonyms-Ghrelin; IsoId=Q9EQX0-1; Sequence=Displayed; Name=2; Synonyms-Gel-Glin4-ghrelin; IsoId=Q9EQX0-2; Sequence=VSP_00134; IsoId=Q9EQX0-2; Sequence=VSP_00134; IsoId=Q9EQX0-2; Sequence=VSP_00134; IsoId=Q9EQX0-1; IsoId=Q9EQX0-1; Sequence=VSP_00134; IsoId=Q9EQX0-1; Inch and Colon. Low expression in the testis and brain. Not detected in the salivary gland, pancreas, liver and lung. Not detected in the salivary gland, pancreas, liver and lung. PTM: O-n-octanoylation is essential for activity (By similarity).
                               hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHRL_RAT STANDARD; PRT; 117 AA.
G90YH7; 09ET69;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 6.3e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-OCTANOATE (BY SIMILARITY).
Missing (in isoform 2).
/FIId-VSP_003246.
EACB49DZB3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMOVED IN MATURE FORM (BY
                                                                                                                                                                                                   Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AJ243503; CAB46500.1; --
EMBL, AB035701; BAB19046.1; --
EMBL, AB060078; BAB2584.1; --
EMBL, AK008658; BAB2584.1; --
EMBL, AK008660; BAB25934.1; --
MGD, MGI.1930008; Ghrl.
GO; GO:000577; C:CYtoplasm; IDA.
GO; GO:00577; C:CYtoplasm; IDA.
INTERPRO: IPR006737; MCIIII_assoc.
INTERPRO: IPR006738; mctliln_assoc.
INTERPRO: IPR006734; mctliln_assoc.
INTERPRO: IPR006741; Preproghrelin.
Féan; PP04643; mctliln_assoc: 1.
Féan; PP04644; mctliln_assoc: 1.
Fean; PP04644; mctliln_ghrelin; I.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA; 13207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.4%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 OQRKESKKPPAKLQPRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
51
117
26
37
                                                                                                                                                 growth regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
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and this statement is not removed.
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modified
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event—Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
Isoid=090YH7-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
Isoid=090YH7-2; Sequence=VSP_003248;
TISSUE SPECIFICITY: Broadly expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, intestine and adipose tissue.

PTW: O-n-octanoylation is essential for activity. The replacement of Ser-26 by aromatic tryptophan preserves ghrelin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hosoda H., Kojima M., Matsuo H., Kangawa K.; "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οĮ
                            Cartus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-21203998; PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y., Ananka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.; "Structure-activity relationship of ghrelin: pharmacological study ghrelin peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASS SPECTROMETRY: MW-3187.1; MW_ERR-0.6; METHOD-Electrospray;
                                                                                                                                   AND ACYLATION OF SER-26.
STRAIN-Sprague-Dawley; TISSUE-Stomach;
MEDLINE-20067959; Pubmed-10604470;
KOJima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa "Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                            Hosoda H., Kojima M., Matsuo H., Kangawa K.; "Purification and characterization of rat des-Gln14-ghrelin, a endogenous ligand for the growth hormone secretagogue receptor. J. Biol. Chem. 275:21995-22000(2000).
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS SPECTROMETRY. AND ACYLALTION OF SER-26. STRAIN-Sprague-Dawley; TISSEE-Stomach; MEDLINE-20357315; Pubmed-10801861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gastrointestinal tissue.";
Biochem. Biophys. Res. Commun. 279:909-913(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blochem. Blophys. Res. Commun. 287:142-146(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANGE-24-36, 38-51.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21433488; PubMed-11549267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21092536; Pubmed-11162448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE-ACTIVITY RELATIONSHIP.
                                                                                                                                                                                                                                          Nature 402:656-660(1999).
 releasing peptide)
                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANGE-24-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>:</u>
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                          pIR; B59316; B59316.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04644; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
ProDom; PB032162; Preproghrelin; 1.
ProDom; Cleavage on pair of basic residues; Signal; Lipoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    /FTId-VSP_003248.
8857546FE51A7691 CRC64;
                                                                                                                                                                                                                                                                                                     Missing (in isoform 2).
                                                                                                                                                                                                                                                                       REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1; Lo
Pred. No. 6.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                      N-OCTANOATE.
              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                       15.4%; Scc.
100.0%; Pre
                                            EMBL; AB029433; BAA89370.1; -. EMBL; AB035699; BAB11956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHRL BOVIN STANDARD; E 09BDJ6; Q9GKY6; 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                36 QQRKESKKPPAKLQPRAL 53
                                                                                                                                                                                                                                                                                                                                    13176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               36 QORKESKKPPAKLOPRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 24-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9913;
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52
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37
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                          VARSPLIC
                                                                                                                 PEPTIDE
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                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms-2;
Name-1; Synonyms-Ghrelin;
Isod-Q9GKY5-1; Sequence-Displayed;
Name-2; Synonyms-del-Gln14-ghrelin;
Isod-Q9GKY5-2; Sequence-VSP_003247;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                             GHRL_PIG STANDARD; PRT; 118 AA.
209CKX5; O9BDG8; O9GKX4,
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                   ö
                                                                                                                                                 Length 116;
                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        -> E (IN REF. 2).
F55536DAC5FA59B6 CRC64;
                                                                                                                                                 DB 1; Le
                                                                                                                                          12.8%; Scor.
100.0%; Pred. No. U. O. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                  InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                             24 50 GH
51 116 RE
26 26 N-1
34 34 K
116 AA; 12792 WW;
EMBL; AF350329; AAK18612.1; -. EMBL; AB035702; BAB19047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB035703; BAB19048.1; -
                                                                                                                                                                                            ULITITITITITI
                                                                                                                                                                                  19 DLAMAGSSFLSPEHQ 33
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                 releasing peptide).
                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                  scrofa (Plg)
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                        rissue-stomach;
                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                     Kojima
                                                                                                                                                                                                                              RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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-1- FUNCTION: TRANSCRIPTIONAL TRANS-ACTIVATOR OF THE GENE (MPRA) FOR THE SMALL NEUTRAL PROTEASE.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                REMOVED IN MATURE FORM (BY SIMILARITY).

MISSING (in isoform 2).

/FTIG=VSP_003247.

L -> P (IN REF. 2; AAR30002).

K -> E (IN REF. 2; AAR30002).

856D3ELD6DABLA76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-A3(2) / M45.
STRAIN-A3(2) / M45.
MEDLINE-21996410; Pubbmed=12000953;
MEDLINE-21996410; Pubbmed=12000953;
MEDLINE-21996410; Pubbmed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarch S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
EMBL; AB035704; BAB19049.1; -.
EMBL; AR20830; AAK19243.1; -.
EMBL; AY208912; AAK19243.1; -.
EMBL; AY208942; AAK1002.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR06741; Preproghrelin.
Pfam; PF04644; motilin_ghrelin; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Probom; PD332162; Preproghrelin; 1.
Probom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small neutral protease regulatory protein.
STREPR OR MPRR2 OR SCO7433 OR SC6D11.29.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA.
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preo. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 L
72 K
12785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 88 :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 DLAMAGSSFLSPEHQ 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100."
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                       Alternative splicing SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
72
118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-1902;
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53
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Gaps

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Indels

Length 344;

DB 1;

6.8%; Sco. 100.0%; Pred. No. 2, 0; Mismatches

G -> AR (IN REF. 2). 485C82C813B52312 CRC64;

344 AA; 37415 MW;

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8; Conservative
                                                                                                      103 RALAGWLR 110
                                                                                          51 RALAGWLR 58
                                                   Local Similarity
            SEQUENCE
CONFLICT
                                     Query Match
                                                                                                                                                                     DP3E_PASMU
                                                                Matches
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Matches
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                                                                                                                                                                     ö
                                                                                                                                                                     Gaps
         InterPro; IPR000847; HTH_LysR.
InterPro; IPR00119; LysR_subst.
Pfam; PF00126; HTH_Li 1.
Pfam; PF03466; LysR_substrate; 1.
PROSITE; PS00049; HTH_LYSR_FAMILY; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DNA_BIND 20 39 H-T+ MOTIF (POTENTIAL).
SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lichenstein H.S., Busse L.A., Smith G.A., Narhi L.O., MacGinley M.O., Rohde M.F., Ratzowitz J.L., Zukowski M.M.; a.Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans."; Gene 111.155-130(1992).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE GENE (SNPA) FOR THE SMALL NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T.; "Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans 66: a novel neutral protease gene with an adjacent divergent putative regulatory gene."; Can. J. Microbiol. 38:912-920(1992).
                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                           Length 328
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M89476; AAA26804.1; ALT_INIT.
InterPro; IPR001847; HTH_LysR.
InterPro; IPR001847; HTH_LysR.
InterPro; IPR00119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00146; HTH_LYSR_SAMILY; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription; DNA-Dinding; Activator.
DNA_BIND 20 39 H-T-H MOTIF (POTENTI
                                                                                                                                        Query Match 6.8%; Score 8; DB 1; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Small neutral protease regulatory protein.
                                                                                                                                                                                                                                                                                    344 AA
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-66 / 1326;
MEDLINE-93099553; Pubmed-1464066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92192468; PubMed-1547948;
                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
EMBL; AL939131; CAB76352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81703; AAA26739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-305 FROM N.A.
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                         103 RALAGWLR 110
                                                                                                                                                                                                                                                                                                                                                                            Streptomyces lividans.
                                                                                                                                                                                            51 RALAGWLR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-1916;
                                                                                                                                                                                                                                                                                                                                                               MPRR OR SNPR
                                                                                                                                                                                                                                                                                  MPRR_STRLI
P43161;
                                                                                                                                                                                                                                                                       MPRR_STRLI
                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                               + (DNA)(N)
-1- SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00929; Exonuclease; 1.
SMART: SW00479; EXOIII; 1.
TIGRFAMS; TIGR00573; dnaq, 1.
TIGRFAMS; TIGRO1406; dnaq, proteo; 1.
TIGRFAMS; TIGRO1406; dnaq, proteo; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
53 AA; 28559 MW; AEF3C48030D4B64C CRC64;
                                           15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DNA polymerase III, epsilon chain (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1;
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                    STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE006046; AAK02190.1; -.
InterPro; IPR0066054; DmaQ.
InterPro; IPR006309; DnaQ.proteo.
InterPro; IPR006055; Exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%;
100.0%; Pre
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                     Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAPFDVG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAPFDVG
                                                                                                                                                                                                                                                  NCBI_TaxID=747;
                                                                                                                                                 DNAQ OR PM0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exonuclease;
DP3E_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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STANDARD;
                                                                                                                                                                           Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                               morphogenesis.";
Mech. Dev. 105:1
                           CHM1_BRARE
P58239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                  CHM1_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII complex. PolIII' sasociates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THE EPSILON SUBUNIT CONTAIN THE EDITING FUNCTION AND IS A PROOFREADING 3-5' EXONUCLEASE (BY SIMILARITY).

CATALYTIC ACTIVITY: N deoxynucleoside Lilphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                STRAIN-Rd / KW20 / ATCC 51907;

STRAIN-Rd / KW20 / ATCC 51907;

MDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGRO0573; dnaq; 1.
TIGRFAMS; TIGRO1406; dnaO_proteo; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ce proteome.
29131 MW; 694C9273AD4438D1 CRC64;
                                                       u1-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase III, epsilon chain (EC 2.7.7.7)
DNAQ OR HI0137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .0%; Score 7; DB 1; 0.0%; Pred. No. 15;
                           256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR006309; DnaQ_proteo.
IPR006055; Exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0°,
100.0%; Pre
                                                     (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00929; Exonuclease; 1.
SMART; SM00479; EXOIII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32699; AAC21808.1; -.
                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006054; DnaQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                          STANDARD;
                                                                                                                   Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B64050; B64050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGR; HI0137;
                                                   01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exonuclease;
                         DP3E_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Best Local
           DP3E_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
1) [Contains: Chondrosurfactant protein (CH-SP)].
LECTI OR CHMI OR CHMI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of zebrafish chondromodulin-1 and expression profile in the notochord and chondrogenic regions during cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NASI_HORVU
ID NASI_HORVU
STANDARD; PRT; 327 AA.

C 02020/9;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDINGG-11429291;
MEDLINE-2122569; PubMed-11429291;
Sachdev S.W., Dietz U.H., Oshima Y., Lang M.R., Knapik E.W., Hiraki Y., Shukunami C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHONDROSURFACTANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (PO
21B377E0348EDDB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHONDROMODULIN-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Scot.
100.0%; Pred. No. ...
0; Mismatches
286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cartilage; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage on pair of basic residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZDB-GENE-010713-1; lectl.
PF04089; BRICHOS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
32235 MW;
                                              16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF322374; AAK77023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
286
49
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170
29
191
286 AA;
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NAPFDVG 104

g 6

NAPFDVG 83

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                               $\text{S482_HUMAN}$ STANDARD; PRT; 464 AA.$\text{AA.}$ Q15428; Q15428; Q15428; Q1-NOV-1997 (Rel. 35, Created)$ 28-FEB-2003 (Rel. 41, Last sequence update)$ $\text{SEP-2003}$ (Rel. 42, Last annotation update)$ $\text{S1610}$ $\text{S1610}$ (S73a66).$$ $\text{S173a66}$; Spliceosome associated protein 62) (SAP S73A2 OR SAP62.$$
                                                                                                                                                                                                                    Cloning of nicotianamine synthase genes, novel genes involved in the
                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-19; 63-69; 181-243 AND 247-266. STRAIN-CV. Ehimehadaka No.1; TISSUE-ROOL; MEDLINE-99137899; Pubmed-9952442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                               Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Tritticeae; Hordeum.
                                                                                                                                                                                        Higuchi K., Suzuki K., Nakanishi H., Yamaguchi H., Nishizawa N.-K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94023929; PubMed-8211113;
Bennett M., Reed R.;
"Correspondence between a mammalian spliceosome component and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAS.
: C476B9622E768816 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: Pyridoxal phosphate.
-1- TISSUE SPECIFICITY: In roots but not in leaves.
-1- INDUCTION: By iron deficiency.
-1- SIMILARITY: Contains 1 NAS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004298; Nicotian_synth,
Pfam; PF03059; NAS; 1.
Transferase; Pyridoxal phosphate; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 7; DB 1
100.0%; Pred. No. 19;
Live 0; Mismatches
                carboxypropyltransferase 1) (HvNAS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB010086; BAA74580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 AA; 35015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity luve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LSPEHOR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||||||
|55 LSPEHQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                             NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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RESIDENCE FROM NA.

RESIDE
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us-09-853-253-2.oli.rsp

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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 EAKEAPA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
242
242
469
475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAKEAPA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUR1_SYNP7
Q55038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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     STITI TERMINATION OF THE PRINCE OF THE PRINC
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A GNRP-11ke gene shares a bidirectional promoter with SAP62

"A GNRP-11ke gene shares a bidirectional promoter with SAP62

"Immediately upstream of AMH.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

"COMPLEX ASSEMBLY FORMED BY THE STADISE BINDING OF US SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSEMIALY. FOR ANCHOR UZ SNRNP TO THE BRANCHPOINT SCOUPLEX.

"IT MAY ANCHOR UZ SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE "E. COMPLEX.

"IT STADING OF SF3A/SAP61, SF3AJ/SAP62, SF3AJ/SAP114. SF3A ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO FORM THE UZ SMALL NUCLEOR RIBONUCLEOPROTEINS COMPLEX (UZ SNRNP).

"SSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO FORM THE UZ SMALL NUCLEOR RIBONUCLEOPROTEINS COMPLEX (UZ SNRNP).

"SSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO FORM THE UZ SMALL NUCLEOR RIBONUCLEOPROTEINS COMPLEX (UZ SNRNP).

"STMILARITY: BELONGS TO THE SF3AZ FAMILY.

"IT SIMILARITY: BELONGS TO THE SF3AZ FAMILY.

"IT SIMILARITY: CONTAINS I MALTIN-TYPE ZINC finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Splicing factor 3A subunit 2 (Spliceosome associated protein 62) (SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dresser D.W., Hacker A., Lovell'Badge R., Guerrier D.; "The genes for a spliceosome protein (SAP62) and the anti-Mullerian hormone (AMH) are contiguous.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                     R GO; GO:0005681; C:spliceosome complex; TAS.
R GO; GO:000334; F:small nuclear ribonucleoprotein; TAS.
R GO; GO:000371; P:mRNA splicing; TAS.
R InterPro: IPR000690; Znf_matrin.
R InterPro: IPR000690; Znf_matrin.
R InterPro: IPR003604; Znf_L01.
R SMART; SM00355; ZnF_C2H2; 1.
R SMART; SM00451; ZnF_U1; 1.
R SMART; SM00451; ZnF_U1; 1.
R SATICEOSOME: MRNA Processing; mRNA splicing; Nuclear protein; Znf_finger; Repeat.
R Zn_FING
SA MATRIN-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 7; DB 1; Length 464; 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
POLY-PRO.
POLY-PRO.
R -> P (IN REF. 1).
FA46F064A55EA2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mol. Genet. 4:1613-1618(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96081226; PubMed-8541848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 29 1
464 AA; 49255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 101 AND 195-196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
HGNC:10766; SF3A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 EAKEAPA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAKEAPA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SF3A2 OR SAP62.
                     GK; Q15428;
MIM; 600796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S3A2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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S3A2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: De novo purine biosynthesis; first step.
-i- SIMILARITY: IN THE C-TERMINAL SECTION: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
-i- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPATase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                            EMBL; X83733; CAC10449.1; -.
MGD; MGI:104912; Sf3a2.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR000504; Znf_Martin.
InterPro; IPR003504; Znf_Martin.
SMART; SM0355; ZnF_C2H2; 1.
SMART; SM0451; ZnF_C11; 1.
PROSITE; PS50171; ZF_MATRIN; 1.
Spliceosome; MRNA processing; mRNA splicing; Nuclear protein; Zinc-finger; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
POLY-PRO.
E8651DC3B0E29C7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.0%; Score 7; DB 3
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  MATRIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U33211; AAA75107.1; -.
PIR; S77612; S77612.
HSSP; P00497; 1A00.
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DR MEROPS; C44.001; -.

DR InterPro; IPR0005834; Amd_phspho_trans.

DR InterPro; IPR0005834; Pary Partiansferase.

DR InterPro; IPR0008393; Pary Partiansferase.

DR InterPro; IPR000836; Partiansferase.

DR InterPro; IPR00180836; Partiansferase.

DR PR03109; Carase_2: 1.

DR Pfam; PF003109; Partiansferase.

DR PROSTIE; PS00103; PurpyRr_PR_TRANSFER; FALSE_NEG.

DR PROSTIE; PS00103; PurpyRr_PR_TRANSFER; FALSE_NEG.

DR PROSTIE; PS001043; Partase; Glycosyltransferase;

RW Purine blosynthesis; Transferase; Glycosyltransferase;

RW Purine blosynthesis; Transferase;

RW Purine blosynthesis; Transferase.

BY SIMILARITY.

T ACT_SITE 27 493 AMIDOPHOSPHORIBOSYLTRANSFERASE.

FT ACT_SITE 27 27 GATASE (BY SIMILARITY).

SQ SEQUENCE 493 AA; 53809 MW; E03508F68922910C CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 110 AKEAPAD 116

Db 299 AKEAPAD 305

Search completed: September 11, 2003, 17:52:38

Job time: 24:2241 secs
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O8dbd4 vibrio vuln O9kpx9 vibrio chol O9cpe0 pasteurella O9lin atreptomyce O95jm5 macaca fasc O8cys mycoplasma O8bw62 mus musculu O8spu3 sus scrofa O8aze salmonella O9419 zea mays (m O8clf mus musculu O8cny4 staphylococ O8lig6 arabidopsis O9line arabidopsis O9lis6 mus musculu O9a6z5 caulobacter O9acz5 caulobacter O9acz2 mus musculu O9cx2 streptococc O8ki24 mus musculu
                                                                                                                                                                                                                                                                                                                                                                            Q8nzr7 streptococc
Q9bdi4 ovis aries
Q95123 sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                          Ogort7 rattus sp.
O9czt0 mus musculu
Q8c3s5 mus musculu
Q9rw31 deinococcus
Q9u2l3 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                             09a0p2 streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.7%; Score 71; DB 4; Length 117; Best Local Similarity 100.0%; Pred. No. 5.5e-65; Matches 71; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025/91; AH25/91.1; -.
InterPro; IPR006/37; motilin_assoc.
InterPro; IPR006/37; motilin_dhelin.
Pfam; PF04643; motilin_ghrelin.
Pfam; PF0464; motilin_ghrelin; 1.
SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                Q8SPU3
Q8AVVO
Q82828
Q941Q8
Q8C1F2
Q8CNY4
Q9LNE6
Q9LNE6
Q9AB53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                               Q9KPX9
Q9CPE0
Q9L1R0
                                                                                                                                                                                                                                                                                                                                            Q8K124
Q9A0P2
Q8NZR7
                                                                                                                               Q8BW62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TAT9;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DGGQAEGAEDE 71
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 Ghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TAT9
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Q8CH53
     Q8TAT9
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Q8ch53 meriones un
Q9r5d1 escherichia
Q81fy4 anguilla ja
Q8av73 gallus gall
Q8v62 streptomyce
Q93zv7 arabidopsis
Q817e4 arabidopsis
Q65529 arabidopsis
Q91063 streptomyce
Q8ff03 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O8hxr4 bos taurus
Q9vdp0 drosophila
Q9xzc4 helicoverpa
Q9i4y8 pseudomonas
                                                                                                       September 11, 2003, 17:46:02; Search time 111.995 Seconds (without alignments) 269.586 Million cell updates/sec
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                                                                                                                                                                                                           1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             830525 segs, 258052604 residues
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                               summaries
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QBCFY4
QBAV73
QBAV52
QBAV52
QB17E4
O65529
Q9L063
Q9L063
Q9KCN5
Q9KCN5
Q9KCN6
Q9YDPO
Q9YDPO
Q9YDPO
Q9YDPO
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Ghrelin precursor.
    NCBI_TaxID=7937;
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                                                                                                                                                                                                                                                                                                SEQUENCE
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SIGNAL
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SIGNAL
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Q8AV73
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA."; Subnitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR4442491; AA006695.1; -
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                                                                                                                                  Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Aggregative adherence fimbria I expression in enteroaggregative Escherichia coli requires two unlinked plasmid regions."; Infect. Immun. 61:1126-1131(1993). SEQUENCE 23 AA; 2403 MW; 688113EAC484CEIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nataro J.P., Yikang D., Giron J.A., Savarino S.J., Kothary M.H.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
14 kDa aggregative adherence fimbriae I protein (Fragment).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.4%; Score 18; DB 11; Length 117; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 18; Conservative 0; Mismatches 0; Indels.
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                  QBCH53;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
    117 AA.
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Best Local Similarity 100.0%; Pred. No. 1;
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    PRT;
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MEDLINE-93162805; PubMed-8094379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 QQRKESKKPPAKLQPRAL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 QORKESKKPPAKLQPRAL 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prepro-ghrelin precursor. GHRELIN.
  PRELIMINARY;
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                                                                                                             Ghrelin preproprotein.
Meriones unguiculatus
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16 IKLSGVQY 23
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                                                                                                                                                                                                                          NCBI_TaxID=10047;
                                                                                                                                                                                                                                                                                                                Ishii H.;
                                                                                                                                                                                                     Meriones
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Q9R5D1
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Q8JFY4
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                  Gaps
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                    TISSUE-Stomach;
Kalya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.,
Kangawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Stomach;

MEDLINE-22181232; PubMed-12193558;

Kalya H., Van der Geyten S., Kojima M., Hosoda H., Kitajima Y.,

Matsumcto M., Geelissen S., Darras V.M., Kangawa K.;

"Chicken girelin: purification, cDNA cloning, and biological activity.";
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Streptiomyces sp. C5.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                        DB 13; Length 111; . 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 116;
                                                                                                                                                                                                                                                                                              0; Indels
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                                                                           "Identification of eel ghrelin.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062427; BAB96565.1; -.
                                                                                                                                                                                                                 7AF95E04DD22DE7B CRC64;
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F5C5FA038F187DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8AV73;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VP52;
01-MRR-2002 (TrEMBLrel. 20, Created)
01-MR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 8; DB 13;
100.0%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA
                                                                                                                                                                                                                                                        6.8%; Score 8; DB 1
100.0%; Pred. No. 3.8
tive 0; Mismatches
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                                                                                                                                                          POTENTIAL.
PROGHRELIN.
                                                                                                                                                                                               GHRELIN-21
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EMBL; AB075215; BAC24980.1; -.
                                                                                                                                                        1 26 PC
27 111 PR
27 48 GH
111 AA; 12831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 AA; 13227 MW;
                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                                                                                                                                                                     23 AGSSFLSP 30
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26 AGSSFLSP 33
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23 AGSSFLSP 30
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A
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                                                                                                                     Q8L7E4
                                                            RESULT 8
Q8L7E4
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"Full Length cDNA of gene Ar4g32720 (GI:7270219).";

"Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AV056237; AAL07086.1;

"InterPro: IPR006344; Lupus_La.

R InterPro: IPR006544; Lupus_La.dom.

R InterPro: IPR006504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                            "Characterization of the Streptomyces sp. strain C5 snp locus and development of an snp-derived expression vector family."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIMIS, PRODOSS, HTHLYSR.
PROSITE; PSO0044; HTH_LYSR_FAMILY; 1.
DNA-binding; Transcription; Transcription regulation.
spenience 313 AA; 34258 MW; C907C8AF5IC3FA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48095 MW; E58EBAF51C35A8F7 CRC64;
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Last annotation update)
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100.0%; Pred. No. 12;
ative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
9;
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100.0%; Pred. No. 9;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                           InterPro: IPR000847; HTH_LysR.
InterPro: IPR005119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF03466; LysR_substrate; 1.
                                                                                                                                                                                                                                                                                                        EMBL; AY072041; AAL61992.1;
                                                                                                                  DeSant1 C.L., Strohl W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 8; Conservative
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SEQUENCE 433 AA; 48(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 RALAGWLR 109
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287 QAEGAEDE 294
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Best Local Similarity
                                                            SEQUENCE FROM N.A.
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NCBI_TaxID-45212;
                                                                                                                                                                                                                                                                              REGULATORS.
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SEQUENCE FROM N.A.

SOUTHWICK A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,

Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

Deng J.M., Hayashizaki Y., Hsuan W.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,

Seki M., Shinn P., Tang C.C., Torcouni M., Wallender E.K., Wong C.,

Theologis A., Davis R.W.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Palm C.J., Bowser L., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Luo S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY136302, AAM96968.1;

EMBL, BY1003996; AAN15715.1;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MG-1998 (TrEMBLrel. 23, Last annotation update)
11-MG-2003 (TrEMBLrel. 23, Last annotation update)
19-pothetical 54.1 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein.
433 AA; 48126 MW; CFFF611A29AA0318 CRC64;
                                                                                                    Created)
Last sequence update)
Last annotation update)
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433
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Interpro; IPR006630; Lupus_La_dom.
Interpro; IPR000504; RNA_rec_mot.
                                         QBL7E4;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00302; LUPUSLA.
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Matches 8; Conservative
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PRELIMINARY;
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SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                Hypothetical protein.
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114 AA.

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MEDLINE-22388234; PubMed-12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S. R., Boutin A., Hackett J., Stroud D.,
Mobley H.L.T., Donnenberg M.S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Extensive mosalc structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.",
EMBL; ARO16764, AAN81560.1;
EMBL; ARO16764, AAN81560.1;
Hypothetical protein; Complete proteome.
SEQUENCE 114 AA; 12611 MW; BFEC5A91285FA0A8 CRC64;
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EMBL; AP001512; BAB05253.1; -. Hypothetical protein; Complete proteome. SEQUENCE 138 AA; 15918 MW; C75EIFDFE5F972FF CRC64; SEQUENCE 138 AA; 15918 MW; C75EIFDFE5F972FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=217992;
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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NCBI_тахID=86665;
                                                                                                                                                                                                                                       Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothettoal protein yfim.
YFIM OR C3111.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-06:H1 / CFT073 / ATCC 700928;
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                               PRT;
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                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli 06
          54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 EVRFNAP 79
              48 DGGQAEG
                                                                                                                                                                                                                  OBFF03;
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Q8FF03
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MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MENTHEY S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kleser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
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Bevan M., Benes V., Rechmann S., Borkova D., Ansorge W., Hoheisel Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 8; DB 10; Length 483; Best Local Similarity 100.0%; Pred. No. 13; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022537; CAA16589.1; -.
EMBL; AL161582; CAB79989.1; -.
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Nature 417:141-147(2002).
EMBL; AL939114; CAB87228.1;
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al protein.
483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC02791.
SC02791 OR SCC105.22C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002344; Lupus_La.
Interpro; IPR006530; Lupus_La.dom.
Interpro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PRO0302; LOPUSLA.
SMART: SM00715; LA: 1.
SMART: SM00360; RRM: 1.
PROSITE: PSS0102; RRM: 1.
Hypothetical protein.
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                                                                                                                                     SEQUENCE FROM N.A.
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Borler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R. Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R. Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R. Lasko P., Ledi Y., Levitsky A.A., Lil J., Lil Z., Liang Y., Lin X.,
R. Liu X., Mattei B. McIntosh T.C., McLeod M.P., McPherson D.,
R. Musko P., Levitsky A.A., Lil J., Lil Z., Liang Y., Lin X.,
R. Markei B. McIntosh T.C., McLeod M.P., McSherson D.,
R. Mantei B. McIntosh T.C., McLeod M.P., McSherson D.,
R. Mantei B. McIntosh T.C., McLeod M.P., Recieb J.M.,
Ran Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ran Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ran Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ran Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ran Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ran Spier E., Stading A.C., Stapleton M., Skupski M.P., Mang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ran Jenner K. W., Romingon M., Zhang G., Zhao Q.A.,
Ran Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu X., Smith H.O.,
Ran Zheng X.H., Zhong F.N., Valorer J.C.;
Ran Jense B.W., Rubin G.M., Venter J.C.;
Ran Jense B.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mazumdar-Leighton S., Babu C.R., Bennett J.;
"Identification of novel serine proteinase gene transcripts in the midguts of two tropical agricultural pests, Scirpophaga incertulas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000).
EMBL. AE003729; AAF5550.1; -
Flybase; Fugn0038781; CG10883
SEQUENCE 143 AA; 14645 MW; 09FE17B83214692B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16933 MW; 1AB9F5115392A319 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; [ Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicoverpa armigera (Cotton bollworm).
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01-NOV-1999 (TrEMBLrel. 12,
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Matches 7; Conservative
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152 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Einspanier R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases EMBL; AJ534389; CAD58880.1; -.
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NON_TER 140 140
SEQUENCE 140 AA; 16076 MW; 0DC51D1517C1A4A6 CRC64;
                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Bone morphogenetic protein receptor IB (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG10883
                                                                                                    140 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression of ovarian growth factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Cumulus oocyte complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Cumulus oocyte complex; Schoenfelder M.;
                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity luv...
7; Conservative
                                                                                                    PRELIMINARY;
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Q8HXR4
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Gaps

0; Indels Best Local Similarity 100.0%; Pred. No. 53; Matches 7; Conservative 0; Mismatches

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2 PSPGTVC 8 |||||||| 89 PSPGTVC 95

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Search completed: September 11, 2003, 17:55:45 Job time: 114.995 secs

Human preproghrell Human PRO1066 poly Human PRO polypept Membrane-bound pro Human PRO1066 poly Human PRO1066 (UNO Human polypeptide Human des-Gln14-gh

human secret secreted/tra PRO polypept

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Human ORFX protein Human exon 3-delet

Title: Perfect score:

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Scoring table: Sequence:

Searched:

Database

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2sig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
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/note= "signal peptide"
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                               ABU59124
ABU59271
ABU59420
ABU60555
ABU58046
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ABU10892
AAY66708
AAY66708
AAB65231
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AAB60517
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AAB60523
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/note= "r
 24-MAR-1997;
24-MAR-1997;
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 Human signal pepti
Human polypeptide
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Zsig33 protein. H
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Human zsig33 prote
Human zsig33 prote
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152.215 Million cell updates/sec
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                                                                      September 11, 2003, 17:21:03; Search time 122.005 Seconds
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2. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

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611
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                             1107863 seqs, 158726573 residues
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(ZYMO ) ZYMOGENETICS INC

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Result Š

Bovine ghrelin pre
Eel ghrelin-like G
Human ghrelin, SEQ
Human ghrelin pept

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes/acids, gastrointestinal inflammation, reflux disease and nutrient carymes, gastrointestinal inflammation, reflux disease and nutrient of absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the chomologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; signal peptide-containing protein; HSPR; diagnosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 611; DB 20;
100.0%; Pred. No. 4.6e-59;
ive 0; Mismatches 0;
                                                                                                                          Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY87236 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0090762.
98US-0094983.
98US-0102686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 117; Conservative
 Sheppard PO;
                           WPI; 1999-070071/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                       N-PSDB; AAX04550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200000610-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
 Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY87236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
AAY87236
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human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anti-inflammatory, antimicrobial, noctropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagoniats of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Antagoniats of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Antagoniats of including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders, (e.g. arterioscierosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's classes, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources.
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                                                                                                                                                                                 YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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100.0%; Pred. No. 4.6e-59;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 168-169; 327pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 2035.
98US-0112129.
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                                                                                          (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
es 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-160673/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ98121
                                                                                                                                                                                     Tang YT,
                                                                                                                                                                                                                                Akerblom IE,
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enzyme; neural development;

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transduction; hormone;
                                                                                                                                                                                                                                                       WPI; 2001-355879/37.
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117; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAF83678
                                                                                                                                   40200138355-A2.
                                                                                                                                                                                             22-NOV-1999;
                                                                                                                                                                                                                                    Sheppard PO,
                                                                   Homo sapiens
                                                                                                                                                     31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
         zsig33;
                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system activity and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemoctactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPSPGTVCSLLLLCMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                               nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                            Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 611; DB 22; 100.0%; Pred. No. 4.6e-59;
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                                                                                                                                                                                           Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                               Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                          such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB62649 standard; Protein; 117
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                                                                                                                                                                                                              Goodrich R,
                                                                                                                                                                                           Asundi V, Wehrman T,
                                                                                 2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0653450.
200US-0653450.
2000US-0653450.
2000US-0653450.
                                                                26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zsig33 polypeptide.
                                                                                                                                                                                                                                  WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                               Zhou P,
                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                                                                           Liu C,
Wang Z,
                                                                                                                                                                                                                                           N-PSDB; AAI58046
                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders
                           WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification
                                                                                                                                                     29-NOV-2000;
         Homo sapiens
                                                                                                                                 14-SEP-2000;
19-OCT-2000;
                                                                                                      09-JUL-2000;
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                                                                                   21-JAN-2000;
                                                                                                                         03-AUG-2000;
                                                                                             25-APR-2000;
                                             26-JUL-2001
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                                                                                                                                                                                                       Wang
                                                                                                                                                                                                               Zhao
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The invention relates to a method of forming a reversible peptide-
creceptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (Comprising residues 24.37
of AAB62649), where the receptor hinds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
cransduction in a cell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of digestive and
parcreatic enzymes and hormones, secretion of insulin like growth factor
c. secretion of non-zsig33 proteins. It is useful for modulating growth
commone secretion in a mammal having a disease associated with abnormal
evels of growth hormone, such as osteoporosis, bone repair, bone
remodeling, low osteoblast levels, cartilage repair and remodeling,
skeletal dysplasia, immune suppression, obesity, growth retardation,
crediction, wound healing and ovulation induction, treating a mammal having
a metabolic disorder requiring neurological feedback, such as satiety
regulation, glucose absorption and metabolism and neuropathy-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastric contractility; nutrient uptake; digestive; pancreatic; human;
insulin-like growth factor-1; growth hormone; bone; gastrointestinal;
glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                           24..37
/note= "specifically claimed fragment that binds to
the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrointestinal disorders, and stimulating glucose induced insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deisher TA, Bishop PD;
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                                                                                                                                                                                                                                                                              Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2000; 2000WO-US32074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0166765
                                                                                                                      G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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AAB60511 standard; Protein; 117 AA.
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                                                       AAB60511;
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    RESULT 6
                AAB6051.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see Secretagoque receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jedjunum tissue, stimulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying.
                                                                                                                       SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating quastric emptying .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                               /label- SGIP_peptide
/note- "this peptide is claimed in Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 611; DB 22; Best Local Similarity 100.0%; Pred. No. 4.6e-59; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishop
                                                                                                                                                                                                                                     24..117
/label- Mature_protein
24..34
/label- SGIP_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delsher TA,
                                                                                                                                                                                                                             /label- Signal_peptide
                                                                                                                                                                                                     Location/Qualifiers
             AAB20101 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000WO-US18306
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SR,
                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO, Jaspers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-123010/13.
N-PSDB; AAF30033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastric emptying
                                                                                           2sig33 protein
                                                                                                                                               therapy; human.
                                                                                                                                                                                                                                                                                                                       WO200100830-A1,
                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999;
                                                                  23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                   04-JAN-2001
                                         AAB20101;
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                                                                                                                                                                                                                Pept 1de
                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                     Peptide
AAB20101
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion collar. The peptides are ghrelin homologues and are concacturised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides. The peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth commone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 4.6e-59;
ive 0; Mismatches 0;
                                                               Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 182; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0210002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2000; 2000WO-JP04907
   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kangawa K, Kojima M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
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                                                                                                                                                                                                                                                                                                                     WO200107475-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1999;
24-APR-2001
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RESULT 7

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ô 셤 ò us-09-853-253-2.rag

(first entry)

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XSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                       Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                                                                                                                                                                    11-MAY-2000; 2000US-203300P.
                                                                                                                                                                                                                                                                     10-MAY-2001; 2001US-0853253.
                                                                                                                                                                                                                                                                                                                                                                                                                  Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                  JASPERS S R. SHEPPARD P O. DEISHER T A.
                                                                             Human zsiq33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-443750/47.
N-PSDB; AAD38238.
                                                                                                                                                                                                                                                                                                                                                                                 BISH/) BISHOP P D.
                                                                                                                                                                                                        US2002055156-A1
                                                                                                                                                                          Homo sapiens
                                              10-SEP-2002
                                                                                                                                                                                                                                       09-MAY-2002
                AAE23838;
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(SHEP/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antique in the production of antibodies against SGIP and in assays to identify modulators of SGIP antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies, agonists and activity of the presence of SGIP in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Short Gastrointestinal Peptide, which has homology to motilin, ful for preventing, diagnosing and treating gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                          Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 611; DB 23; 100.0%; Pred. No. 4.6e-59;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 39-40; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deisher TA,
                                                                                                                                                                                                                               /note= "signal peptide"
                                                                                                                                                                                                                                                                  "mature protein"
                                                                                                         Amino acid sequence of a human zsig33
                                                                                                                                                                                                        Location/Qualifiers
              ABB78319 standard; Protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                99US-141592P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheppard PO, Jaspers SR,
                                                                             (first entry)
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                                                                                                                                                                                                                                                 24..119
/note= "r
                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-634794/68.
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Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABV72214
                                                                                                                                                                         Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1999;
                                                                                                                                                                                                                                                                                                  US6420521-B1
                                                                         05-DEC-2002
                                                                                                                                                                                                                                                                                                                                  16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                            ABB78319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
ABB78319
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Deisher TA, Bishop PD;

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The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones.

The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZsiG33 expression.

The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZsiG33 peptides are used as antiques in need of restorative therapy. The ZsiG33 and in assays to identify modulators of ZsiG33 expression and activity. The anti-ZsiG33 antibodies and also used as diagnostic agents for detecting the presence of ZsiG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide is used in protein therapy. The present sequence
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Disclosure; Page 27; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
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AAE23838 standard; Protein; 117 AA.

AAE23838 ID AAE2 RESULT 8

ò 8 ð a us-09-853-253-2.rag

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Homo sapiens.
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14-SEP-1998;
14-SEP-1998;
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29-0CT-1998;
29-0CT-1998;
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10-SEP-1998;
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17-SEP-1998;
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20-APR-1999;
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02-DEC-1999;
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                    Sequence
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ABU66790
     X OS
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                                                                                                                                                                                                                                                                                                                        The invention relates to zsigl3-like peptides (zS33LP) including 2sigl33-linker, zsigl33-beta, zsigl3-gamma, zsigl33-delta and zsigl33-linker, zsigl33-beta, zsigl33-gamma, zsigl33-delta and csigl33-linker, zsigl33-beta, zsigl33-gamma, zsigl33-delta and czsigl33-like peptides. ZS33LP peptides actimizedels encoding such czsigl33-like peptides. ZS33LP peptides actimized the immune system in boosting immunity to infectious diseases, treating immunocompromised in patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines of the invention are used to identify and improving of ingrowth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate consultation of tumour cells, as additives to anti-chypoglycaemic preparations containing glucose and as adsorption containing glucose and as adsorption containing glucose and as adsorption containing cluckers for oral drugs which require fast nutrient action and to standard contractions of tissues associated with gastrointestinal system, brain and central nervous system. These contections are useful for treating discontest are useful for treating discontest as and/or and contractility in vivo and to treat contractines are useful for treating discontest as associated with mastrointestinal and growth related diseases. ZS33LP peptides, nucleic with mastrointestinal contractility in sorreition of the careful or with any or the contractility in the discontine and contractility and disc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones in the pancreas and/or brain, gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises asign3-like peptides -
                                                                                                                                                                    Human; zsig33-like peptide; Zs33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; anthypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation;
                                                                                                                                                                                                                                                                                                                                                                      /note= "Human mature zs1g33 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishop PD;
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                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide 24..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 80-81; 89pp; English.
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                 AAE15883 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2001; 2001WO-US15091.
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                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                      Human zsig33 protein.
                                                                                                                                                                                                                                        IIV; zsig33 protein.
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N-PSDB; AAD25759.
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                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                   26-MAR-2002
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                                                                  AAE15883;
                                                                                                                                                                                                                                                                                                       Key
Peptide
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RESULT 9
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                                                                                                   1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPF 60
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                                                                                                                                                                     61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                      61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human; PRO polypeptide; secreted and transmembrane protein; tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder;
                                 Length 117;
                                                                  Indels
                           ; DB 23;
4.6e-59;
thes 0;
                                                                   Mismatches
                                 Score 611;
Pred. No. 4
                                                                                                                                                                                                                                                                                  ABU66790 standard; Protein; 117 AA
                               100.0%; Sc
100.0%; Pr
tive 0;
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98WO-US19094.
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98WO-US18824
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99WO-US28564
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                Matches 117; Conservative
                               Query Match
Best Local Similarity
117 AA;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides for linking bloactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists. Cor modulating blological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the human polypeptides of the invention.

Or pro polypeptides of the invention.

Or pro polypeptides of the invention was obtained in electronic format directly from the USPTO website at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                  therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
                                  New secreted and transmembrane PRO nucleic acids, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 611; DB 24;
100.0%; Pred. No. 4.6e-59;
11ve 0; Mismatches 0;
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                                                                                                    Claim 12; Fig 442; 660pp; English.
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98WO-US12456.
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98WO-US17888.
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Matches 117; Conservative
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N-PSDB; ACA03823
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14-JUL-1998;
28-AUG-1998;
10-SEP-1998;
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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20010S-0808689
20010S-0818689
20010S-0828366
20010S-0854208
20010S-0860218
20010S-0860218
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20010S-0866034
20010S-0874503
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2000WO-US34956.
2001WO-US06520.
2001WO-US06666.
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2000WO-US00376.
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2001US-0924419.
2001US-0927796.
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2000WO-US08439.
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2001US-0796498
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11-FEB-2000;
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25-MAY-2001;
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310-MAR-2000;
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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature
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AL, Sherwood S;
ood WI, Zhang Z;
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1, Godowski PJ, Gurney AL, Shel
umas D, Watanabe CK, Wood WI,
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                                                                                        2001US-0872035.
2001US-0874503.
2001US-0882636.
2001US-0886342.
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       2001US-0796498.
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2001US-0924419
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2001US-0931836.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
                                                                                                                                                                                                                                                                                        aging, AIDS, or cancer
                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                     WPI; 2003-331925/31.
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05-APR-2001;
10-MAY-2001;
18-MAY-2001;
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16-AUG-2001;
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       28-FEB-2001;
09-MAR-2001;
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Claim 12; Fig 442; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleaties sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host calls for producing PRO proteins, PRO fusion proteins, anti-PRO attracellular domains and mature sequences, methods of detecting PRO proteins, PRO included are vectors and host calls for producing PRO proteins, and mature sequences, methods of detecting properties factor alpha from human blood.

Thr-alpha (tumour necrosis factor alpha) from human blood, and the proliferation of differentiation of chondrocyte cells, the release of proliferation of, or gene expression in pericyte cells, the release or proteing cells, the proliferation of T-lymphocyte cells, the release of proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FRP) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of a method for detecting the properties are useful for treating inflammatory diseases, organ polypeptides are useful for treating inflammatory diseases, organ and a company of the nucleotide sequences cited above. The nucleic organical control or and a supportation of all municip probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, blosensors or bloreactors. Both are useful in tissue typing. The present sequence represents a PRO protein of the invention.

AA; Seguence Score 611; DB 24; Length 117; Pred. No. 4.6e-59; 100.0%; 100.0%; Best Local Similarity Query Match

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            Human; PRO; hypertrophy of neonatal heart; anglogenesis; wound healing;
                                       cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; vEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
Gaps
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Wood WI, Zhang Z;
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ME, Goddard A, Godowski PJ, Gurney A
Stewart TA, Tumas D, Watanabe CK, Wo
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23.AUG-2000;
24.AUG-2000;
08.NOV-2000;
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21.AUR-2001;
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30-DEC-1999;
31-EEB-2000;
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22-FEB-2000;
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21-MAR-2000;
31-MAR-2000;
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02-MAR-2000;
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Gerritsen N
Smith V, S
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Gao W;

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04-JUN-1998;
04-JUN-1998;
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  The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in inking a bloomstive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus collypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus stimulate adrenal cortical capillary endothelial growth, and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO136, PRO136, PRO136, PRO136, Induce c-fos in endothelial growth, and PRO136, useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular calothelial growth in cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO136 pro136 and PRO1375 stimulate proliferation of endothelial cells and shiph would be PRO136 stimulate proliferation of endothelial cells and shiph would be proliferation of endothelial cells and shiph would be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stimulated T-1ymphocytes and are therapeutically useful for enhancing immune response. PROB28, PROB26, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/Prol1feration of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries; e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce prol1feration of mammallan kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the prol1feration and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This
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                                                          Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the amino acid sequence of a novel human PRO protein.
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nes 117; Conservative
WPI; 2003-148238/14.
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                 N-PSDB; ABX89361
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Matches
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dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in comparing a bloadcative molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cuseful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO5136, PRO4136 and PRO1367. PRO41360 and PRO1387 induce c-fos in endothelial growth, and PRO5136, CC PRO413, PRO828, PRO826, PRO819, PRO1126, PRO1387 induce c-fos in endothelial cells, and are thus useful for treating cancerous tumours. PRO812 inhibits vascular conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular condothelial growth in cells and is thus useful for inhibiting endothelial cell growth in condothelial growth in condothelial growth in condothelial growth in condothelial cells and is thus useful for inhibiting tumour growth. PRO826, PRO184, PRO184, PRO8184, PRO826, PRO1068 or PRO1132 enhances survival profiteration of stimulated T-lymphocytes and are therapeutically useful for renating retinal condothers of injurles, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 end disorders of injurles, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and therefore are useful for treating kidney disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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              9805 - 088033 P
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1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPF 60
                                                                                                                                                                          1 HPPGTVCSLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                                                                                                                                                                                                              61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                         decreased mesangial cell function such as Berger disease or other nephropathles associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.
                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; PRO; secreted; transmembrane; pharmaceutical;
diagnostic; blosensor; bloreactor; tumour; therapeutic;
gene therapy; tumour-associated antigenic target; TAT; ADEPT;
antibody-dependent enzyme mediated prodrug therapy; cytostatic.
                                                                                                             Length 117;
                                                                                                                                    Indels
                                                                                                             100.0%; Score 611; DB 24; 100.0%; Pred. No. 4.6e-59;
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                                                                                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein, #108.
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                                                                                                         Query Match
Best Local Similarity 100."
Matches 117; Conservative
                                                                                      Sequence 117 AA;
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Paoni NF;
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                                                                                                                                      Gaps
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                                                                                                     Length 117;
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                                                                                                  100.0%; Score 611; DB 24; 100.0%; Pred. No. 4.6e-59;
                                                                                                                                  0; Mismatches
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98US-100634P.
98US-100858P.
98US-113296P.
99US-123957P.
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2000WO-US06319.
2000WO-US06884.
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                                                                                                Query Match 100.08 Best Local Similarity 100.08 Matches 117; Conservative
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10-MAR-2000;
15-MAR-2000;
16-SEP-1998;
17-SEP-1998;
22-DEC-1998;
12-MAR-1999;
23-JUN-1999;
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98US - 090349P.
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98US - 090658P.
98US - 09069P.
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                     Score 611; DB 24;
Pred. No. 4.6e-59;
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                                   0; Mismatches
                     100.0%;
100.0%;
98US-097986P.
98US-098014P.
                    Query Match 100.
Best Local Similarity 100.
Matches 117; Conservative
26-AUG-1998;
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Search completed: September 11, 2003, 17:25:02 Job time : 124.005 secs

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Gaps

29483, A 20969, A 8, Appli 4, Appli 20326, A 12, Appl 12, Appl 12, Appl 12, Appl 12, Appl 12, Appl

Sequence 5
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Sequence 2
Sequence 4
Sequence 2
Sequence 2
Sequence 2
Sequence 1
Sequence 1
Sequence 1
Sequence 1
Sequence 1

Appli Appl Appli Appli

Run on:

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Query Match 100.0%; Score 611; DB 3; Best Local Similarity 100.0%; Pred. No. 4.1e-67; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Saattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09046479
; Patent No. 6291653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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MOLECULE TYPE: prot
FRAGMENT TYPE: inte
  USA
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ZIP: 98102
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  \begin{array}{c} \text{constant} \\ \text{constan
  Sequence 4, Appli
Sequence 5, Appli
Sequence 25, Appli
Sequence 1, Appli
Sequence 21192, A
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Sequence 27192, A
Sequence 2719, A
Sequence 27132, A
Sequence 27133, A
Sequence 2, Appli
Sequence 17420, A
Sequence 17420, A
Sequence 2553, A
Sequence 2553, A
Sequence 2763, A
Sequence 2763, A
Sequence 2763, A
Sequence 2763, A
Sequence 2760, A
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Sequence 268, App
                                                                                                                                                                                                   (without alignments)
158.243 Million cell updates/sec
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                                                                                                                                                                      September 11, 2003, 17:21:03 ; Search time 31.2834 Seconds
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2: /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
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5: /cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-27419
US-09-252-991A-27327
US-09-252-991A-28102
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US-09-252-921A-17420
US-09-252-991A-24713
US-09-252-991A-25653
US-09-252-991A-17073
US-09-252-991A-18600
US-09-252-991A-18600
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US-09-252-991A-23192
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US-09-046-479-4
US-08-822-897C-4
US-09-608-810A-5
US-09-029-213B-25
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US-08-416-581B-5
US-08-416-581B-5
US-09-087-465-6
US-09-526-542-2
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US-08-416-581B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Result No.

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Gaps

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Length 117;

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1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.1e-67;
Matches 117; Conservative 0; Mismatches 0; Indels (
              APPLICANT: Jaspers, Stephen R.
APPLICANT: Deisher, Theresa A.
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/996,243 CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268, Application US/09996243
Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eaton, Dan L.
                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-996-243-268
                                                                                                                                                                                                                                                                      LENGTH: 117
                                                                                                                                                                                                                                                  SEQ ID NO 4
                                                                                                                                                                                                                                                                                           TYPE: PRT
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MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
                     1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
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                                                                                                    61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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100.0%; Pred. No. 4.1e-67;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                         Sequence 2, Application US/08822897C Patent No. 6380158 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seat!
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98102
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                                                                                                                                                                                                      US-08-822-897C-2
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186

Sequence 4, Application US/09608810A Patent No. 6420521

RESULT 3 US-09-608-810A-4

GENERAL INFORMATION:

Gaps ö

1997-11-12 NUMBER: 60/065311 1997-11-13 NUMBER: 60/06570 1997-11-24 1998-02-25 NUMBER: 60/078910 1998-03-20 NUMBER: 60/078910 1998-03-20 NUMBER: 60/08910 1998-04-28 NUMBER: 60/084600 1998-05-07 NUMBER: 60/084600 NUMBER: 60/084600 NUMBER: 60/084600 NUMBER: 60/084600	NUMBER: 6 1998-06- 1998-06- 1998-06- NUMBER: 6 1998-06- 1998-06- NUMBER: 6	0008873 0008873 10008873 100088873 10008882 10008882 10008885 111 10008886 10008886 10008886 10008886 10008886 10008886 10008886
FILING DATE: APPLICATION APPLICATION FILING DATE: APPLICATION APPLICATION APPLICATION APPLICATION	PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION ILING DATE PPLICATION PPLICATION ILING DATE	DATE DATE DATE DATE DATE DATE DATE DATE
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PRIOR APPLICATION NUMBER: 60/089519
PRIOR FILING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PL

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26 SFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIK 85
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                                                                                             Length 119
                                                                                           Ouery Match 14.1%; Score 86; DB 3; Length 119
Best Local Similarity 26.0%; Pred. No. 0.0067;
Matches 20; Conservative 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
OPERARIE: FASTSEQ FOR WINGOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
FLING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Disher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08822897C Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               : | :: | :|
89 MDSRQLEKYRATLERLL 105
                                                                                                                                                                                                                                                                    86 LSGVQYQQHSQALGKFL 102
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SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                 internal
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserve
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        ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-046-479-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 611; DB 4; Best Local Similarity 100.0%; Pred. No. 4.1e-67; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Delsher, Theresa A.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/09154
PRIOR PAPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091639
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PELING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091639
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFRENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09046479
Patent No. 6291653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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2 PSPGTVCSLLLLGMLWLDLAMAGSSFL---SPEHQRVQQRKESKKPPAKLQPRALAGWLR 58
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                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                           201 LSTEAQDTLISIKNQLNQRLSNAQTQQVSAKLQIFIEDNLIQETYDNPLDK 251
                                                                                                                                                                                                                                                                                                     82 ------VGIK-----LSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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                                                                                                                            DB 3; Length 323;
0.99;
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                                                                                                                                                                      36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,827
FILING DATE: 21-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/USJP/02661
FILING DATE: 25-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 327328/1994
FILING DATE: 28-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W., Suite 800 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 72.5; DB 1;
Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MIYADERA KAZULAKA
APPLICANT: YAMADA, YUJI
APPLICANT: TAKEBAYASHI, YUJI
APPLICANT: ATKIYAMA, Shinichi
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHPITE
STPPET
                                                                                                                            Query Match 11.9%; Score 73; DB 3
Best Local Similarity 27.9%; Pred. No. 0.99;
Matches 31; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/POCKET NUMBER: 0-42514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08696827
Patent No. 5798213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.98;
24.48;
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TELEFAX: (202) 293-7860
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 244 amino acids amino acid
  323 amino acids
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Best Local Similarity 24.49
Matches 30; Conservative
                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-029-2138-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2: D.C.
IRY: U.S.A.
20037
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MOLECULE TYPE: pep
    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-696-827-1
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Patent No. 6180098
GENERAL INFORMATION:
GENERAL INFORMATION:
TTLLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: MCDERMOLE, Will & Emery
STREET: 600 13th Street, NW
CITT' Washington
STATE: District of Columbia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
14.1%; Score 86; DB 4; Length 119;
Best Local Similarity 26.0%; Pred. No. 0.0067;
Matches 20; Conservative 19; Mismatches 38; Indels
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                                                                                                                                                           APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Dalsher, Thereas A.
APPLICANT: Dalsher, Thereas A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 60/141,592
PRIOR APPLICATION NUMBER: 60/141,592
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
FROM NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    Sequence 5, Application US/09608810A Patent No. 6420521 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH HYOSUK KIM
REGISTRATION NUMBER: 41,425
REFERENCE/DOCKET NUMBER: 5017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8000
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89 MDSRQLEKYRATLERLL 105
  MDSRQLEKYRATLERLL 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-756-8087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Sus scrofa
US-09-608-810A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-029-213B-25
                                                                                  -09-608-810A-5
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Sequence 27419, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION: Rated al.
GENERAL INFORMATION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: A BRUGIANGA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
WUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 PRHRRCCYNGCAYACLEAVPPPVLDWLVQPKPRWLGGNGWLLDGPEEVLQAEACSTTED 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 GGOSQGAEDQPGRTGGDRRDTDGQRRHPRRRLDHRHRRQQQPPHPLNIRRGGRRAVRRTF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 PEHQR-----VQQRKESKKPPAKL-----QPRALA--GWL--RPEDGGQAE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GAEDEL----EVRFNAPFDV--GIKLSGVQYQQHSQALGKFLQDILWEEAKE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.5%; Score 70; DB 2; Length 220; Best Local Similarity 32.7%; Pred. No. 1.4; Matches 37; Conservative 10; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5; DI
Pred. No. 1.8;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-27327; Sequence 27327, Application US/09252991A; Sequence 27327, Application US/09252991A; Patent No. 6557795; Patent INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34012.6
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US-09-252-991A-27419
                                                                                                     REGISTRATION NUMBER: 35,723
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GGQAEGAEDE-----
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11.4%;
Best Local Similarity 24.1%;
Matches 20; Conservative
                                     FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                             TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-27419
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 PEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHS---QALGKFLQDILWEEA-KEAP 114
                                                                                                                                                      54 AVVNGSAQGAQIGAML------MAIRLRGMDLEETSVLTQALAQSGQQLEWPEAWROOL 106
1:11 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 |
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APPLICANT: ROWLEY, DAVID R.
APPLICANT: ROWLEY, UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens & Glichtist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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11.9%; Score 72.5; DB 4; Length 773;
Best Local Similarity 28.7%; Pred. No. 3.7;
Matches 25; Conservative 8; Mismatches 29; Indels 2
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ----- GGQAEGAEDELEVRFNAP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23192, Application US/09252991A Patent No. 6551795
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STREET: 1100 Louislana, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                   115 ADK 117
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US-09-252-991A-23192
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92

Gaps

99

Gaps

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Query Match
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.118 APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR RAPLICATION NUMBER: US 60/074,788 PRIOR RAPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUM
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US,60/222,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28102

LENGTH: 406
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11.3%; Score 69; DB 4; Length 406;
Best Local Similarity 20.9%; Pred. No. 4.1;
Matches 28; Conservative 19; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.4%; Score 69.5; Di
Best Local Similarity 28.4%; Pred. No. 2.8;
Matches 31; Conservative 14; Mismatches
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US-09-130-242-2
Sequence 2, Application US/09130242B
; Patent No. 6194558
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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EDAIEAMGREALAE 276
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US-09-252-991A-28102
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COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-997-573-268
US-09-991-172-268
US-09-997-726-268
US-09-997-559-268
US-09-997-601-268
US-09-990-443-268
                                                                                                                                                                US-09-989-734-268
US-09-997-653-268
US-09-997-653-268
US-09-997-628-268
US-09-997-666-268
US-09-990-438-268
US-09-990-562-268
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US-09-989-726-268
US-09-998-156-268
US-09-990-437-268
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US-09-997-683-268
US-09-989-729A-268
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US-09-997-514-268
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STREET: 1201 Eastlake Avenue East
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APPLICATION NUMBER: 09/046,479
FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09794987 Patent No. US20010041791A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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COUNTRY: USA
ZIP: 98102
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                                                                                                                    US-09-794-987-2
Sequence 2, Appl 1
Sequence 268, Appl Sequence 268,
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Sequence 2, Appli
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239.348 Million cell updates/sec
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1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117
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2: 'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.ppp:*
3: 'cgn2_6/ptodata/1/pubpaa/DSO7_WEW_PUB.ppp:*
4: 'cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
5: 'cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
6: 'cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
6: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
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11: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
12: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
13: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
14: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
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16: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
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13: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-989-731-268
US-09-991-073-268
US-09-991-163-268
US-09-991-163-268
US-09-991-604-268
US-09-991-456-268
US-09-992-598-268
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US-09-989-723-268
US-09-989-279-268
US-09-989-277-268
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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100.0%; Score 611; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.7e-60;
Matches 117; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.7e-60;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHEPPARD, PAUL
APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
TILE OF INVENTOR: Zsig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT APPLICATION NUMBER: 05/203,300
PRIOR PILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 2
LENTH: 117
              TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 268, Application US/09989722 Patent No. US20020072067al GENERAL INFORMATION:
LENGTH: 117 amino acids
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Patent No. US20020055156A1
GENERAL INFORMATION:
APPLICANT: JASPERS, STEPHEN
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Forgy, Sherman
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Best Local Similarity 100.0°
Matches 117; Conservative
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; ORGANISM: Homo sapiens
US-09-853-253-2
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: P2730PLC63 CURRENT APPLICATION NUMBER: US/09/989,722 CURRENT FILICE DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
Grimaldi, J. Christopher
                                                                                                                          Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                          Gurney, Austin L.
                                                           Kljavin, Ivar J.
Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090445
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PRIOR PELING DATE: 1998-06-34
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08810
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-11
PRIOR PRIOR FILING DATE: 1998-06-11
PRIOR PRILAGION NUMBER: 60/08861
PRIOR FILING DATE: 1998-06-11
PRIOR PRILCATION NUMBER: 60/08976
PRIOR FILING DATE: 1998-06-12
PRIOR PRILCATION NUMBER: 60/08976
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR PELING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-23
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PRIOR PLING DATE: 1998-06-17
APPLICATION NUMBER: 60/088738
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1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60 61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117 Gaps ö Length 117; 0; Indels Ouery Match 100.0%; Score 611; DB 9; Best Local Similarity 100.0%; Pred. No. 6.7e-60; Matches 117; Conservative 0; Mismatches 0; R APPLICATION NUMBER: 00/050240
R APPLICATION NUMBER: 60/090542
R APPLICATION NUMBER: 60/090557
R APPLICATION NUMBER: 60/09057
R APPLICATION NUMBER: 60/090676
R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690 RELIENG DATE: 1998-06-25

RAPELICATION NUMBER: 60/090695

RETLING DATE: 1998-06-25

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RETLING DATE: 1998-06-26

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RETLING DATE: 1998-06-26

RETLING DATE: 1998-07-01

RETLING DATE: 1998-07-02

RETLING DATE: 1998-07-07

RETLING DATE: 1998-07-07 Sequence 268, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Baket Kevin P. Fong, Sherman Gerber, Hanspeter Gertitsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Ferrara, Napoleone Desnoyers, Luc Eaton, Dan L. US-09-989-723-268 APPLICANT:
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R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08876
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R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-16
R PILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/089947

R RELING DATE: 1998-06-19

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R APPLICATION NUMBER: 60/089952

R APPLICATION NUMBER: 60/089952

R APPLICATION NUMBER: 60/090246

R FILING DATE: 1998-06-19

R PILING DATE: 1998-06-22

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R APPLICATION NUMBER: 60/090429
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R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-18
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                    APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-10
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PLG2

CURRENT APPLICATION NUMBER: US/09/989,723

CURRENT FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-01-17

PRIOR APPLICATION NUMBER: 60/06531

PRIOR APPLICATION NUMBER: 60/06530

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-20

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R FILING DATE: 1998-04-28

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R APPLICATION NUMBER: 60/087106

R APPLICATION NUMBER: 60/087607

R FILING DATE: 1998-06-02

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R APPLICATION NUMBER: 60/087609

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R APPLICATION NUMBER: 60/08781

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088021

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R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088738
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                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                         Paoni, Nicholas F.
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Kljavin, Ivar J.
                       Napier, Mary A.
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TT: Stewart, Timothym.
TT: Tumas, Daniel
TW Watanabe, Colin K.
TW Williams, P. Mickey
TT: Wood, William I.
                     Roy, Margaret Ann
 Paon1, Nicholas F
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                                         PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090678
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
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PRIOR PELING DATE: 1998-07-07
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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/090542
            FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Forny, Sherman
APPLICANT: Forny, Sherman
APPLICANT: Gerber, Hanspeter
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Best Local Similarity 100.0
Matches 117; Conservative
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Napier,Mary A.
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/088888
PRIOR APPLICATION NUMBER: 60/08861
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
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R FILING DATE: 1998-06-17
R PRILICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
R FILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/089532
R APPLICATION NUMBER: 60/089538
R APPLICATION NUMBER: 60/089598
R R PILING DATE: 1998-06-17
R PELLING DATE: 1998-06-17
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RILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
APPLICATION NUMBER: 60/089908
APPLICATION NUMBER: 60/089908
RILING DATE: 1998-06-18
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NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090435

NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090444

RFILING DATE: 1998-06-24
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FILLING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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FILLING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILLING DATE: 1998-06-19
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/08826
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
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PRIOR PAPLICATION NUMBER: 60/090694
PRIOR PELING DATE: 1998-06-25
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PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
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PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091682
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09178
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09178
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07 Query Match
Best Local Similarity 100."
Matches 117; Conservative 셤 δ ö

US-09-989-727-268

Sequence 268, Application US/09989727 Patent No. US20020072497A1 GENERAL INFORMATION: Eaton, Dan L. Ferrara, Napoleone Gerber, Hanspeter APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David Desnoyers, Luc Fong, Sherman APPLICANT: APPLICANT: APPLICANT: APPLICANT

Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. Kljavin, Ivar J. Gerritsen, Mary E. Goddard, Audrey Napier, Mary A. APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT

Roy, Margaret Ann Stewart, Timothy A Paoni, Nicholas F. APPLICANT:

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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
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R APPLICATION NUMBER: 60/090254
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R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
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A APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

A PRILICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17
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RILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/090431

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090435

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R APPLICATION NUMBER: 60/090444
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R APPLICATION NUMBER: 60/090445
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                           APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-Ub-24
APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/089512
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                                                       APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Sanng, Fer Zanng, Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFRENCE: P270PLG5
CURRENT FILING DATE: 1907-10-17
PRIOR APPLICATION NUMBER: US/09/989,727
CURRENT APPLICATION NUMBER: US/09/989,727
PRIOR PELICATION NUMBER: US/09/989,727
PRIOR PELICATION NUMBER: US/09/989,727
PRIOR PELICATION NUMBER: US/09/989
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PRIOR PELICATION NUMBER: US/09/989
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PRIOR FILING DATE: 1998-06-04
PRIOR PPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/088217
PRIOR APPLICATION NUMBER: 60/088217
PRIOR PLING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/088655

R FILING DATE: 1998-06-09

R APPLICATION NUMBER: 60/088734

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088742
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                      Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
  Tumas, Daniel
APPLICANT:
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OR FILING DATE: 1998-06-05

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OR APPLICATION NUMBER: 60/088212

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OR APPLICATION NUMBER: 60/08655

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OR FILING DATE: 1998-06-09

OR APPLICATION NUMBER: 60/088734

OR APPLICATION NUMBER: 60/088734

OR APPLICATION NUMBER: 60/088734

OR APPLICATION NUMBER: 60/088736

OR APPLICATION NUMBER: 60/08874

OR APPLICATION NUMBER: 60/08810

OR APPLICATION NUMBER: 60/08810
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FILING DATE: 1998-06-10
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100.0%; Pred. No. 6.7e-60;
1ve 0; Mismatches 0;
                                                              PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR PELING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/090662
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/09154
PRIOR PELING DATE: 1998-07-02
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Av1 J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090678
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Grimaldi, J. Christopher
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Williams, P. Mickey
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Stewart, Timothy A.
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                            LING DATE: 1998-06-25
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Gerber, Hanspeter
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Best Local Similarity 100.0
Matches 117; Conservative
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
PRIOR PAPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08976
PRIOR APPLICATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/089514
PRIOR APPLICATION NUMBER: 60/089514
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
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PRIOR APPLICATION NUMBER: 60/09044
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PRIOR PELING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1908-06-24
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PRIOR APPLICATION NUMBER: 60/08953
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PRIOR APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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PRIOR APPLICATION NUMBER: 60/090355
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PRIOR PPLICATION NUMBER: 60/090429
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PRIOR APPLICATION NUMBER: 60/090431
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PRIOR APPLICATION NUMBER: 60/090435
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PRIOR APPLICATION NUMBER: 60/090540
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PRIOR APPLICATION NUMBER: 60/090676
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PRIOR APPLICATION NUMBER: 60/089908
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OR FILING DATE: 1998-06-25

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OR PLING DATE: 1998-06-25

OR APPLICATION NUMBER: 60/090695

OR APPLICATION NUMBER: 60/090863

OR FILING DATE: 1998-06-26

OR APPLICATION NUMBER: 60/090863

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OR PILING DATE: 1998-07-01

OR PILING DATE: 1998-07-02

OR PILING DATE: 1998-07-07

OR PILING DATE: 1998-07-07 Conservative Query Match Best Local Similarity Matches 117; Conserv PRIOR g ò

Sequence 268, Application US/09989732 Patent No. US20020123463A1 GENERAL INFORMATION: Grimaldi, J. Christopher Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Ferrara, Napoleone APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L. Godowski, Paul JS-09-989-732-268 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Pan, James Paoni, Nicholas F. Napier, Mary A. Danie APPLICANT APPLICANT

Gurney, Austin L.

Kljavin, Ivar J.

APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

9,732		
ON: Acids Encoding to P2730P1C57 TION NUMBER: US/09/989 ATE: 2001-11-19 ATE: 2001-11-19 ATE: 2001-11-19 ATE: 1997-06-16 N NUMBER: 60/062186 E: 1997-11-12 N NUMBER: 60/065311 E: 1997-11-12 N NUMBER: 60/066770 E: 1997-11-24 N NUMBER: 60/066770 AN NUMBER: 60/066770 AN NUMBER: 60/066770 BE: 1997-11-24 N NUMBER: 60/066770		NUMBER: 60 1998-06-0 1998-06-0 1998-06-0 1998-06-0 1998-06-0 1998-06-0 1998-06-0 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1098-06-1 1098-06-1
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PRIOR APPLICATION NUMBER: 06/089512

PRIOR PELING DATE: 1998-06-16

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R APPLICATION NUMBER: 66/062250

R FILING DATE: 1997-10-17

RAPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

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R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/06770

R FILING DATE: 1997-11-24
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R APPLICATION NUMBER: 60/08/609
R PILING DATE: 1998-06-02
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R PAPLICATION NUMBER: 60/08789
R FILING DATE: 1998-06-03
R PILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/078910
FILLING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-04-28
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION UNDBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/086033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088202
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APPLICATION UNDBER: 60/088217
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/088861
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; Pred. No. 6.7e-60;
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PRIOR APPLICATION NUMBER: 60/091860
PRIOR PELING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
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R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-26
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R FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/090695
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Gurney, Austin L.
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100.0%;
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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Best Local Similarity 100.0
Matches 117; Conservative
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Godowski, Paul
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Eaton, Dan L.
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US-09-991-073-268
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R APPLICATION NUMBER: 60/089532
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
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R APPLICATION NUMBER: 60/089908
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R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/090696
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
                                                                              FILING DATE: 1998-06-16
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1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60 61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PL08
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16 ö Length 117; Indels Score 611; DB 10; Pred. No. 6.7e-60; ); Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/09154
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09159
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07 Sequence 268, Application US/09990442 Patent No. US20020132252A1 GENERAL INFORMATION: Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Query Match 100.0%; S Best Local Similarity 100.0%; P Matches 117; Conservative 0; Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey Ferrara, Napoleone Gerritsen, Mary E. Fong, Sherman Gerber, Hanspeter Gurney, Austin L. Kljavin,Ivar J. Napier,Mary A. APPLICANT: Ashkenazi, Avi J Botstein, David Desnoyers, Luc Eaton, Dan L. Pan,James RESULT 10 US-09-990-442-268 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT  $^{\mathrm{q}}$ δ g ŏ

PRIOR PELICATION NUMBER: 60/06250
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PRIOR PELICATION NUMBER: 60/08102
PRIOR PELICATION NUMBER: 60/08103
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUBBER: 60/089512
PRIOR PELICATION NUBBER: 60/089514
PRIOR PLINK DATE: 1998-06-17
PRIOR PLINK DATE: 1998-06-18
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PRIOR PLINK DATE: 1998-06-18
PRIOR PLINK DATE: 1998-06-19
PRIOR PLINK DATE: 1998-06-23
PRIOR PLINK DATE: 1998-06-23
PRIOR PLINK DATE: 1998-06-23
PRIOR PLINK DATE: 1998-06-24
PRIOR PLINK DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PRIOR TILING DATE: 1997-11-24
PRIOR PRIOR CATION NUMBER: 60/076945
PRIOR PRIOR CATE: 1998-02-25
PRIOR PRIOR DATE: 1998-02-25
PRIOR PRIOR DATE: 1998-02-25
PRIOR PRIOR DATE: 1998-03-25
PRIOR PLICATION NUMBER: 60/08106
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PRIOR PLICATION NUMBER: 60/08759
PRIOR PLICATION NUMBER: 60/08759
PRIOR PLICATION NUMBER: 60/08759
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-07
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PRIOR APPLICATION NUMBER: 60/08021
PRIOR PLING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08021
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PRIOR APPLICATION NUMBER: 60/08021
PRIOR PLING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/08021
PRIOR APPLICATION NUMBER: 60/08030
PRIOR APPLICATION NUMBER: 60/08030
PRIOR PLING DATE: 1998-06-10
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PRIOR PRIOR DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08036
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PRIOR PRIOR DATE: 1998-06-10
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                        DR FILING DATE: 1997-11-13

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DR FILING DATE: 1997-11-24

DR APPLICATION NUMBER: 60/06570

DR FILING DATE: 1998-02-25

DR APPLICATION NUMBER: 60/078910

DR FILING DATE: 1998-03-20

DR FILING DATE: 1998-03-20

DR FILING DATE: 1998-03-20

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/084600

DR APPLICATION NUMBER: 60/084600

DR PILING DATE: 1998-05-28

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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding, the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 6.7e-60;
11ve 0; Mismatches 0;
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CURRENT FILING DATE: 2001-11-14
                                                                                  NR FILING DATE: 1998-07-01

NR APPLICATION NUMBER: 60/091478

NR APPLICATION NUMBER: 60/091544

NR FILING DATE: 1998-07-01

NR FILING DATE: 1998-07-01

NR FILING DATE: 1998-07-01

NR APPLICATION NUMBER: 60/091519

NR APPLICATION NUMBER: 60/091626

NR APPLICATION NUMBER: 60/091626

NR APPLICATION NUMBER: 60/091633

NR FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R FILING DATE: 1998-07-09
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Patent No. US20020132253A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/049787
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                                                              APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/090863
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Gurney,Austin L.
Kljavin,Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
                                  1998-06-26
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Paoni, Nicholas F.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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nes 117; Conserv
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PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
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PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR APPLICATION NUMBER: 60/089601
PRIOR PILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR PILING DATE: 1998-06-18
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PRIOR PELING DATE: 1998-06-18 R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/09044

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R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090355

R FILING DATE: 1998-06-23

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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION WUMBER: 60/089532 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090853 PFLING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-06-19 FILING DATE: 1998-06-25 PRIOR

1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE Gaps ö Length 117; Indels 100.0%; Score 611; DB 10; 100.0%; Pred. No. 6.7e-60; 0; Mismatches DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091544

OR FILING DATE: 1998-07-01

OR APPLICATION NUMBER: 60/091519

OR APPLICATION NUMBER: 60/091626

OR FILING DATE: 1998-07-02

OR APPLICATION NUMBER: 60/091633

OR FILING DATE: 1998-07-02

OR APPLICATION NUMBER: 60/091978

OR APPLICATION NUMBER: 60/091978

OR PILING DATE: 1998-07-07

OR APPLICATION NUMBER: 60/091978

OR PILING DATE: 1998-07-07

OR PILING DATE: 1998-07-07

OR PILING DATE: 1998-07-07 Sequence 268, Application US/09993604 Patent No. US20020137075A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J. Grimaldi, J.Christopher Gurney, Austin L. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I. PRIOR APPLICATION NUMBER: 60/09:
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 Ferrara, Napoleone Paoni, Nicholas F. Gerber, Hanspeter Gerritsen, Mary E. Godowski, Paul J. Kljavin, Ivar J. Conservative Baker, Kevin P. Botstein, David Napier, Mary A. Goddard, Audrey Desnoyers, Luc Fong, Sherman Eaton, Dan L. Query Match Best Local Similarity Matches 117; Conserv Pan,James US-09-993-604-268 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-13
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NUMBER: 60/066770 1997-11-24 NUMBER: 60/075945 1998-02-25 1998-03-20 1998-03-20 NUMBER: 60/08332 1998-04-28 NUMBER: 60/084600 1998-05-20 1998-05-20 NUMBER: 60/08700 1998-05-20 NUMBER: 60/08700	ER: 60/08/75 ER: 60/08/75 ER: 60/08/82	NUMBER: 60/08878 1998-06-10 NUMBER: 60/088742 1998-06-10 NUMBER: 60/088824 1998-06-10 NUMBER: 60/088826 1998-06-10 NUMBER: 60/08858 1998-06-11 1998-06-11 NUMBER: 60/08876 1998-06-11 1998-06-11 NUMBER: 60/08976 1998-06-11 NUMBER: 60/08976 1998-06-11 NUMBER: 60/08976 1998-06-12 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089514
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R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/08332
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APPLICATION NUMBER: 60/089440
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PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065311
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Patent No. US20020137890a1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Goddard, Audrey
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Kljavin, Ivar J.
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APPLICATION UNMBER: 60/091544
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APPLICATION NUMBER: 60/091519
APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06570
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PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091632
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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; Sequence 268, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
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Grimaldi, J.Christopher
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Best Local Similarity 100.
Matches 117; Conservative
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Pan, James
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PRIOR PELICATION UNDREES: 60/081322
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PRIOR APPLICATION NUMBER: 60/08759
PRIOR PILLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08025
PRIOR APPLICATION NUMBER: 60/08021
PRIOR PILLING DATE: 1998-06-03
PRIOR PILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08026
PRIOR PELLING DATE: 1998-06-04
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PRIOR PELLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-05
PRIOR PILLING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/08960
PRIOR PAPLICATION NUMBER: 60/08963
PRIOR APPLICATION NUMBER: 60/08961
PRIOR PAPLICATION NUMBER: 60/08901
PRIOR PAPLICATION NUMBER: 60/08901
PRIOR PAPLICATION NUMBER: 60/08907
PRIOR PAPLICATION NUMBER: 60/08907
PRIOR PAPLICATION NUMBER: 60/08904
PRIOR PAPLICATION NUMBER: 60/08904
PRIOR PILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION UNBARE: 60/081705
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-06-02
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Janay, Semin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1203
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020160384Al
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/084600
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William in
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Gerber, Hanspeter
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US-09-992-598-268
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Q91177 human immun
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Q91604 gescherichia
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Q80831 mus musculu
Q91847 arabidopsis
Q8155 homo sapien
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.7%; Score 609; DB 4; Length 117; 99.1%; Pred. No. 3.1e-58; ive 1; Mismatches 0; Indels
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Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025/91; AAH25/91.1;
InterPro; IPR006/38; motilin_assoc.
InterPro; IPR06738; motilin_assoc.
Fram: PF04643; motilin_assoc; 1.
Pfam: PF04644; motilin_assoc; 1.
Pfam: PF04644; motilin_ghrelin; 1.
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08GD25
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01-JUN-2002 (TrEMBLrel. 21,
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Ghrelin.
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Matches 116; Conservative
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                                                                                                                             1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Q8PFF9
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Gapop 10.0 , Gapext 0.5
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10 ILLLSILGTETALAGSSFLSPTYKNIQQQKDTRKPTARLHRRGTESFW----DTDETEGE 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                   Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                                        Ishii H.;
"Nucleotide sequence of the Mongolian gerbii preproghrelin mRNA.";
"Nucleotide sequence of the EMBL/GenBank/DDBJ databases.
EMBL; AF442491; AA006965.1;
"SEQUENCE 117 AA: 13035 MW; 27657687FC026A74 CRC64;
                                                                Meriones ungulculatus (Mongollan jird) (Mongollan gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaiya H., Van der Geyten S., Kojima M., Hosoda H., Kitajima Y.,
Matsumoto M., Geelissen S., Darras V.M., Kangawa K.;
"Chicken ghrelin: purification, cDNA cloning, and biological
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                                                                                                                                                                                                                                 84.3%; Score 515; DB 11; Length 117;
82.1%; Pred. No. 4.8e-48;
iive 8; Mismatches 13; Indels (
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F5C5FA038F187DE9 CRC64;
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Endocrinology 143:3454-3463(2002).
EMBL; AB075215; BAC24980.1; -.
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116 AA; 13227 MW;
                    01-MAR 2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Ghrelin preproprotein.
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Warches 96; Conservative
PRELIMINARY;
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                                                                                                    Meriones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                          Q8AV73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
Q8AV73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygil; Neopterygil; Teleostel; Ostarlophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-222448; Pubmed-12239128; Unniappan S., Lin X., Cervini L., Rivier J., Kaiya H., Kangawa K., Peter R.E.; "Goldfish ghrelin: molecular characterization of the complementary "Goldfish ghrelin: molecular characterization of the complementary actimulatory role in food intake."; Endocrinology 143:4143-4146(2002). EMBL; AF454389; AAN16215.1; -. SEMBL; AF454390, AAN16215.1; -. SEQUENCE 103 AA, 11520 MW; 0881343BDCD0C012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWE-EAKE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaiya H., Kojima M., Hosoda H., Riley L.G., Hirano T., Grau G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.9%; Score 146; DB 13; Length 111; llarity 38.1%; Pred. No. 4.4e-08; Conservative 19; Mismatches 29; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL, AB062427; BAB96565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHRELIN-21.
7AF95E04DD22DE7B CRC64;
                                         01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-0cr-2002 (TrEMBLrel. 22, Last annotation update)
Prepro-ghrelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23, Created)
23, Last sequence update)
23, Last annotation update)
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111 AA
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PRT;
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                                                                                                                                                                          Anguilla japonica (Japanese eel).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of eel ghrelin.";
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27 111 PR
27 48 GH
111 AA; 12831 MW;
PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Matches 43; Conserv
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                                                                                                                                                                                                                                                                           NCBI_TaxID=7937;
                                                                                                                                                                                                                                                                                                                                                       rissue-stomach;
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12.9%;
27.6%;
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                            Waterston R.;
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Q8PFF9
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7 VCSLLLLGMLWLDLAMAGSSFLSPEHORVQORKESKKPPAKLQPRALAGWLRPEDGGQAE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VCSLLLLGMLWLDLAMAGSSFLSP-EHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 LCAL----SICVESVKGGTSFLSP------AQKPOGRRPPRM------GRRD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Stomach;
MEDLINE-21538897; PubMed-11546772;
Kalya H., Kojima M., Hosoda H., Koda A., Yamamoto K., Kitajima Y.,
Matsumoto M., Minamiteke Y., Kikuyama S., Kangawa K.;
"Bullfrog Ghrelin Is Modified by n-Octanoic Acid at Its Third
Threonine Residue.";
                                                                                  67 GAEDELEV-----RFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKE 112
                                                                                                              Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 14.2%; Score 87; DB 13; Length 114; Local Similarity 27.9%; Pred. No. 0.11; es 29; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 EGAEDEL---EVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDIL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AA; 12756 MW; 1FE419ACB30AA141 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Preproghrelin precursor.
Rana catesbelana (Bull frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibla; Batrachia; Anura; Neobatrachia; Ranoldea;
                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 135.4 kDa protein.
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BULLFROG GHRELIN-28.
BULLFROG GHRELIN-27.
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NCBI_TaxID=6239;
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EMBL; AB058510; BAB71718.1; -.
                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-8400;
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Matches
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SEQUENCE FROM N.A.

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STRAIN=306 / ATCC 13902 / XV 101;

MEDINR=2202145; PubMed-12024217;

A BALVE S. P. PubMed-12024217;

A BALVE S. M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A ALVES L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Raratu J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratuyama A.M., Kishi L.T., Leller R.P., Lemos B.G.M., Lemos M.V.F.,

Ratsuyama A.M., Kishi L.T., Leller R.P., Lemos E.G.M., Lemos M.V.F.,

Ratsuyama A.M., Kishi L.T., Leller R.P., Lemos E.G.M., Lemos M.V.F.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Ratina H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Taratta M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

A Spinola L.A.F., Tarita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

Tromparison of the genomes of two Xanthomonas pathogens with differing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GGQAEGAEDELEVRFNAPFDVGIKLSGV----QYQQHSQALGKFLQDILWEEAKEA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 PPQQ------QYMYPGPSAQGLSMQQIAAIQQQQQHQQ-----YQQRILLQQQQQQA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae; Xanthomonas.
YCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
                                                                                                                                                                                                                                                                             "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U97194; ABB52447.2; -.
WormPep, C37A2.2; CE27747.
Hypothetical Protein.
SEQUENCE 1239 AA; 135436 MW; 81F6C299FDC77D85 CRC64;
STRAIN=Bristol N2;
Le T.T., Kemp K., Scheet P.;
"The sequence of C. elegans cosmid C37A2.";
submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC4024.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 79; DB;
; Pred. No. 13;
20; Mismatches
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Nature 417:459-463(2002).
Hyptchetical protein; Complete proteome.
SEQUENCE 119 AA; 12971 MW; AAD76860E
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MEDLINE-ZUGSD'IT; PUDDMEG=1091034 A. Abreu F.A., Acencio M., Alwarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccoral E.D., Bordin S., Bove J.M., Briones M.R.S., Buenco M.R.P., Camargo C.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferreira J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Futlan L.R., Roper J.E., Kuramae E.E., Langate E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Langet E.C., Kitajima J.P., A Krieger J.E., Kuramae E.E., Langet F., Lambais M.R., Leite L.C.C., A Machae B.M. J. Martins E.M.F., Marino C.L., Mardeira A.M.B.N., Madeira M.R., Machae J.B., Mandeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Mandeira A.M.B.N., Martins E.M.F., Matsukuma A.Y., Mandeira M.C., de Oliveira R.C., Palmieri D.A., Paris A., A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., A de Souza A.P., Roberto P.G., Santelli R.V., Sawasaki H.E., A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., A zago M.A., Zatz M., Meidanis J., Sotubal J.C., Sawasaki H., Wa zaluz M.A., Verlooski-Almelda S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Sotubal J.C., Sawasaki H. E., BEBL, Aberose of the plant pathogen Xylella fastidiosa."; The genome sequence of the plant pathogen Xylella fastidiosa."; The genome sequence of the plant pathogen Xylella fastidiosa."; The plant pronse; IPR000252; DedA.
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbacch J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Hypotherical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                         12.3%; Score 75; DB 16; Length 158; 38.6%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                            27 FLSPEHQRVQQRKESKKPPAK - - LQPRALAGWLRPEDGGQAEGA 68
                                                                                                                                                                                                                                                                                                                                                                                                  11 protein; Complete proteome.
158 AA; 17814 MW; C9BA42BF9C10E1BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Xf0277.
                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00597; DedA;
Pfam; PF01569; PAP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kylella fastidiosa.
                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2371;
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09PGM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
09PGM1
        δ
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SLCRARQVALVALWVAMAAPSAWGQGYPWVQSGREALPPSARGNSRTLSDTIRHVQRSTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 SPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                          63 GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPA 115
                                                               || || || GOILGAE-----RVPFDGG-NLNRVKYMKDGRVHTVYEP----EQTQAAPA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBXW90;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Hypothetical protein RSc2585.

RSC2585 OR RSO0797.

Ralstonia solanacearum (Pseudomonas solanacearum).

Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00368; FADPNŘ.
PRINTS; PR00411; PNDRDTASEI.
FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SEQUENCE 410 AA; 45112 MW; 76630BEBEDBFF4C CRC64;
                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                        Q9HSO1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Vng0468c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.5; DE
Pred. No. 8.8;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| : | : |
131 VKYDGDEEVYGDIID 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 VQYQQHSQALGKFLQD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-64091;
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Q8XW90

RESULT 10 Q8XW90

Matches

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RKA STAIN-BERELEX;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Cawley S., Derman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brotsteir P., Brotcher P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Boriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
RA Liu X., Mattel B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nakon K., Nixon K., Nixskern D.R., Percel J.M.,
RA Roller R., Reliagon K.A., Nixon K., Nixskern D.R., Percel J.M.,
RA Roller R., Reliagon K.A., Nixon K., Nixskern D.R., Percel J.M.,
RA Roller R., Reliagon K.A., Nixon K., Scheeler F., Shen H.,
RA Charler B., McIntosh T.C., Scheeler F., Shen H.,
RA Charler B., McIntosh T.C., Scheeler F., Shen H.,
RA Charler B., Scheeler R., Scheeler F., Shen H.,
RA Charler B., Scheeler R., Scheel
                                                                                            9
                                                                                                                                                               422 GALASLIGFARLYLGAHWLSDVLGGMLFGIFWLLVLGIAYRRRLTHELQVNPLSWLFYGT 481
                                                                                                                                                                                                                        78
                                                                                                                                                                                                   28 -----LSPEHQRVQQRKESKKPPAKLQPRALA--GWLRPEDGGQAEGAEDELEVRFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.Y., Wassariam D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
                                                                                            Gaps
                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                       Length 709;
                                                                                            Indels
 11 protein; Complete proteome.
709 AA; 79163 MW; 0EAA922E4B463318 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                       DB 16;
                                                                                                                                                                                                                                                                        79 PFDVGIKLSGVQYQQHSQALGKFLQ-DILWEEA 110
                                                                                                                                                                                                                                                                                             359 AA
                                                   r Match 12.0%; Score 73.5; I Local Similarity 23.5%; Pred. No. 28; Pred. 36; Conservative 14; Mismatches
                                                                                                                            5 GTVCSL----LLLGMLWLDLAMAGSSF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG2958 protein (HL05328P) (LP02926p).
LECTIN-24DB OR CG2958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-7227
Hypothetical
SEQUENCE 7(
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
Q9VQX3
                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunnimalayaan M., Stevenson D.M., Zhou Y., Vary P.S.;
"Analysis of the replicon region and identification of an rRNA operon on pBM400 of Bacillus megaterium OM B1551.";
Mol. Microbiol. 39:1010-1021(2001).
EMBL; AF142677; A819594.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 534 AA; 60110 MW; 816057052FA159DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kromiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                         STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003577; AAF51038.1; -.

EMBL; AX1061025; AAL28573.1; -.

EMBL; AX119000; AAM50860.1; -.

HSSP; P22897; 1EGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 359 AA; 41546 MW; 1895E525594584C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 60.1 kDa protein.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 DVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPAD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 73; DB 5; 28.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
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MEDLINE-21150449; Pubmed-11251820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0040102; lectin-24Db.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9RPV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09RPV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
Q9RPV9
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                                                                                                                                                       35 -- VQQR----KESKK-----PPAKLQPRALAGWLR---PEDGGQAEGAEDELEVRFN- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQR--VQQRKESKKPPAKLQPRALAGWLRPE 60
   ---- 34
                                 | |||| ::: :|| | || || 349 TTWGLLLLAKIFMINAVGVGTILIREHLRKNDSPSLTKFLMSDVSFMLIIVLIVGTIAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhalerao R.P., Sivertzon M., Sterky F., Lundeborg J., Sandberg G.;
"The role of Rb-related protein from hybrid aspen in wood formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Populus tremula x Populus tremuloides.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Asteridae, lamilds, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tumor suppressor gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB01221; BAA76477.1;
HSSP: 906400; LGUX.
InterPro; IPR005670; Cyclin.
InterPro; IPR005720; RB_A.
InterPro; IPR007719; RB_B.
Pfam; PF01888; RB_A; I.
Pfam; PF01887; RB_B; I.
SMART; SM00385; CYCLIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 AA; 106602 MW; 0138DE06FC89ED2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NTRD1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Retinoblastoma-related protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      961 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1035 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQ 90
                                                                                                                                                                                                                                                                         78 -- APFDVGIKLSGVQYQQHSQALGKFLQ 103
6 TVCSLLLLGMLWLDLAMAGSSFLSPEHQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sekine M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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25 SSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGI 84
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                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                               Length 1035;
                                                                                                                                                                                                                                                    33; Indels
                                                                            InterPro; IPR002720; RB_A.
InterPro; IPR002719; RB_B.
Pfam; PF01854; RB_A; 1.
SMART; SM00387; RB_B: 1.
SMART; SM00385; CYCLIN; 1.
SEQUENCE 1035 AA; 114608 MW; F66191BF50BAAAA5 CRC64;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133675; AAF61377.1; -.
HSSP; P06400; 1GUX.
                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: September 11, 2003, 17:30:24
ne : 115.369 secs
                                                                                                                                                                                                             Score 73;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                       765 KLAAVRINGMIEKLQPSQQH 784
                                                                                                                                                                                                                                                                                                                                                                  85 KLSGVQY------QQH 94
                                                                                                                                                                                                               11.9%;
                                                            InterPro; IPR006670; Cyclin.
                                                                                                                                                                                                                               Best Local Similarity 35.0 Matches 28; Conservative
                                                                                                                                                                                                                 Query Match
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Job time
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25687, A 4, Appli 4, Appli

19, Appl 17695, A 2, Appl 1, Appl 1, Appl 10, Appl 23, Appl 24, Appl 24, Appl 21, Appl

Sequence

ALIGNMENTS

Sequence Seq

Run on:

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US-09-252-991A-25687

US-09-464-483-4

US-09-464-483-4

US-09-252-991A-32421

US-09-252-991A-22896

US-09-252-991A-17695

US-09-252-991A-17695

US-09-252-991A-17695

US-09-267-388-2

US-08-81-601-1

US-08-81-601-1

US-08-81-176-1

US-08-81-176-1

US-08-81-176-1

US-08-81-176-1

US-08-81-176-1

US-08-81-176-1

US-09-207-388-23

US-09-207-388-22

US-09-207-388-22

US-09-207-388-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              US-09-046-479-2
 0000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
Sequence 2, Appli
Sequence 4, Appli
Sequence 268, App
Sequence 2033, Ap
Sequence 2033, Ap
Sequence 2036, A
Sequence 113, Appl
Sequence 11, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26333, A Sequence 17300, A Sequence 1, Appli Sequence 1, Appli
                                                                                                                  (without alignments)
123.627 Million cell updates/sec
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                                                                                                  September 11, 2003, 17:48:42; Search time 8.2139 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*
            GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-996-243-268
US-09-134-011C-3033
US-09-252-991A-27032
US-09-252-991A-20368
US-09-252-991A-16798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-32089
US-09-252-991A-26333
US-09-252-991A-17300
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US-09-198-452A-612
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US-08-403-852D-31
US-08-510-646B-32
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-231-818-31
US-09-135-994-12
                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                           US-09-853-253-4
24
1 ALAGWLRPEDGGQAEGAEDELEVR
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                 0
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                                                                      OM protein
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                                                                                                                                                                                             Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 24; DB 3; 1 Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          ZOUNTIL USA ZIONATE COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                         APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SANISIAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
Sequence 2, Application US/09046479 Patent No. 6291653 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
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Result ģ Sequence 18951, A Sequence 30162, A Sequence 6794, Ap Sequence 33000, A Sequence 33000, A Sequence 2, Appli

US-08-396-650-1 US-08-768-626-1 US-09-252-991A-18951 US-09-252-991A-30162

US-09-328-352-6794 US-09-252-991A-33000

US-09-266-965-120 US-09-252-991A-29569

2, Appli 120, App Sequence 120, App Sequence 29569, A ö

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC13
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                             Length 117;
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                                                                                                                                                                                                                                                                           100.0%; Score 24; DB 4; 1
100.0%; Pred. No. 2.1e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: US/04/996,243
CURRENT FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/078945
PRIOR FILING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
                   PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                    52 ALAGWLRPEDGGQAEGAEDELEVR 75
                                                                                                                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEVR 24
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Grimaldi,J.Christopher
Gurney,Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
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Goddard, Audrey
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J.
Napier, Mary A.
  PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eaton, Dan L.
                                                                                                                                              ORGANISM: Homo saptens
                                                                                                                                                                                       ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-996-243-268
                                                                                                      LENGTH: 117
                                                                                   SEQ ID NO 4
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Similarity 100.0%; Pred. No. 2.1e-16;
24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FSSESSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
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Patent No. 6420521
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: DeliAnt: Theresa A.
APPLICANT: Blshop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
                                                                                                                                                                               APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: TORESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                        1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                                                                                                                                              Sequence 2, Application US/08822897C Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SAWISIAK, Deborah A
RECISTRATION NUMBER: 97-0
FELECOMHUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 117 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                      STREET: 1201 E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                        US-08-822-897C-2
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Best Local
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5-07 60/087106 5-28 60/087607 6-02 60/08759 6-02 60/087827 6-03 6-03 6-04 6-04	6-04 60/088028 60/088029 6-04 6-04 6-04 6-04 6-04 6-04 6-07 6-08823 6-07 6-08823 6-07 6-08821 6-07 6-08821 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-08821 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-07 6-	10101010101010101
	1998 - 0 NUMBER:	1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER: 1998-0 NUMBER:
FILING DATE APPLICATION FILING DATE PRICATION FILING DATE APPLICATION FILING	ILLING DATE PELICATION ILLING DATE ILLING DATE PELICATION ILLING DATE	FILIC CARRELL CONTROL CARRELL CONTROL CARRELL
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PRICOR APPLICATION NUMBER: 60/08963
PRIOR PELICATION NUMBER: 60/08901
PRIOR PELICATION NUMBER: 60/08901
PRIOR PELICATION NUMBER: 60/08907
PRIOR PELICATION NUMBER: 60/08907
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-13
PRIOR PELING DATE: 1998-06-14
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-07-01
PRIOR PELING D

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield and AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 37;
tive 0; Mismatches
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; Pred. No. 24;
0; Mismatches
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; Sequence 16798, Application US/09252991A
; Patent No. 6551795
                                                                                                                                     Sequence 20368, Application US/09252991A Patent No. 6551795
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; Patent No. 5624894
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Best Local Similarity 100.
Matches 7; Conservative
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383 GGQAEGA 389
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DGGQAEG 28
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                                                                                                                                                                                                                                                                                                                                                           Sequence 3033, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 552
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                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 19;
iive 0; Mismatches
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100.0%; Pred. No. 23;
tive 0; Mismatches
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3033
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 66/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 66/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100..
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Matches 7; Conservative
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US-09-252-991A-27032
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US-09-134-001C-3033
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APPLICANT: Jacques, Nathalle
APPLICANT: Jacques, Patricia
APPLICANT: Lacrolx, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                   COUNTRY: USA

LIF: 2000-315

COMPUTER: USA

COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
NAME: MEYERERECE/DOCKET NUMBER: 03806.0054-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 6; DB 2;
100.0%; Pred. No. 47;
iive 0; Mismatches
         STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/08510646B Patent No. 6077699
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 QAEGAE 18
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US-08-403-852D-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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VENTION: Polypeptides Involved In The
VENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                            NUMBER OF SECUENCE:
CORRESPONDENCE BUTCHS.
ADDRESSE:
ADDRESSE:
BUTCHS.
CITY: Alexandria
STATE: P.O. Box 1404
CITY: Alexandria
STATE: P.O. Box 1404
CITY: Alexandria
STATE: P.O. Box 1404
COUNTRY: United States
ZIP: 2213-1404
COMPUTER: ELBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: Z7-ARR-1995
CLASSIFICATION NUMBER: 26,254
ATTORNEY/ARDIALON NUMBER: 26,254
REFERENCE/COCKET NUMBER: 26,254
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acid
STRANDEDNESS: Single
TOPLOAGY: Ilnear
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); OTHER INFORMATION: /note= "Position 30 = Glu-NH2.
US-08-428-488-13
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OTHER INFORMATION: /note= "Position 1 = H-Ser.
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Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanch, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Lacroix, Patricia
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Tagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
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OTHER INFORMATION: /note-
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Best Local Similarity 100.
Matches 6; Conservative
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MOLECULE TYPE: peptide
FEATURE:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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26 GAEDEL 31
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Gaps
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TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REPERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A
CURRENT FILING DATE: 2000-10-06
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 09/135,994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09135994A
Patent No. 6280938
GENERAL INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REPERENCE: University of Minnesota
CURRENT APLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SSETUTOR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 6; DB 3; 100.0%; Pred. No. 47;
                                                                                                                                                                                                   03806.0054-00000
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100.0%; Pred. No. vo.
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                    FILING DATE: 10-MAY-1995
APPLICATION UNMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
    US/08/403,852
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                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 408-4400
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 97 amino acids
TYPE: amino acids
STRANBENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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57 RPEDGG 62
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2 QAEGAE 7
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US-09-231-818-31
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US-09-684-843A-12
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APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 97;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 6; DB 3;
Pred. No. 47;
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                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILIG DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
PRICING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
FILING DATE: 25-SEP-193
PRIOR APPLICATION DATA:
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
                                                           APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/231,818
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100.0%; Pre
0; '
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Thibaut, Denis
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Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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APPLICANT: Blanc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y: USA
20005-3315
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US-08-510-646B-32
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 15
US-09-198-452A-612
Sequence 612, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: GITIffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PRILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 612
LENGTH: 183
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25.0%; Score 6; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels
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; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PALENLIN VAR. 2.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-684-843A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-612
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| 155 AEGAED 160
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57 RPEDGG 62
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September 11, 2003, 17:27:22; Search time 25.2834 Seconds (without alignments) 150.669 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            1107863 seqs, 158726573 residues
                                                                                                                                                                                                                      24
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                                                                        OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                        OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                            US-09-853-253-4
24
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A Geneson 19.Tunn3. Database :

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ä	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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 m	/SIDS1/gcgdata/geneseg/genesegp-emb1/AA1982.DAT:*
	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
 2	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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12:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13:	/SIDS1/gcgdata/geneseg/genesegp-embl/AA1992.DAT:*
14:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15:	/SIDS1/gcgdata/geneseg/genesegp-emb1/AA1994.DAT:*
16:	/SIDS1/gcgdata/geneseq/genesegp-embl/AA1995.DAT:*
17:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19:	/SIDS1/gcgdata/geneseg/genesegp-emb1/AA1998.DAT:*
<b>5</b> 0:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21:	/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*
55:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24:	/SIDS1/qcqdata/qeneseq/qenesegp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human zsiq33-linke	Human zsiq33-linke	Human exon 3-delet	Human des-Gln14-qh	Protein designated	Human signal pepti	Human polypeptide	Human zsiq33 polyp	Zsig33 protein. H
SUMMARIES	ΩI	AAE23839	AAE15884	AAE33410	AAB60517	AAW87991	AAY87236	AAM38890	AAB62649	AAB20101
	DB	23	23	24	22	20	21	22	22	22
	Query Match Length DB	24	24	91	116	117	117	117	117	117
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	24	24	24	24	24	24	24	54	24
	Result No.	1	~	m	∢	'n	9	7	80	O

Human ghrelin prep Amino acid sequenc	33		ユ	Human secreted/tra	Novel secreted and	Novel human secret	Human secreted/tra	Novel human secret	Human secreted/tra	Human PRO polypept	Human sectreted/tr	Human preproghreli	Human PRO1066 poly	Human PRO polypept	Membrane-bound pro	Human PRO1066 poly	_	èp	33-1	33	÷	Human zsig33-linke	e F	ø	ø	Arabidopsis thalia	SnpR activator pro	Amino acid sequenc	Staphylococcus ep1	Drosophila melanog	Human peptide #168	PD-1_Ctail2 peptid	PD-1-related pepti	Neutrophil-activat
AAB60511 ABB78319	AAE23838	AAE15883	ABU66790		ABU59871	ABU59124	ABU59271	ABU59420	ABU60555	ABU58046	ABU58977	AAE33409	ABU13937	ABU10892	AAY66708	AAU12392	AAB65231	AAM40676	AAE23840	AAE23841	AAE15885	AAE15886	AAB60523	AAG29677	AAG29676	AAG29675	AAW36129	AAB30494	ABP38188	ABB66948	AAM96893		185	AAY50239
22	23	23	24	24	24	24	24	24	24	24	24	24	24	24	21	22	22	22	23	23	23	23	22	21	21	21	19	21	23	22	22	24	74	20
117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	118	118	118	126	23	23	23	23	83	334	428	483	311	311	442	1931	14	56	26	39
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.8	95.8	95.8	95.8	41.7	33,3	33.3	33,3	29.5	29.5	29.5	29.5	25.0	25.0	25.0	25.0
	24																			23		23	10	80	æ	80	7	7	7	7	9	9	9	9
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37			40		42	43	44	

## ALIGNMENTS

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Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                              Location/Qualifiers
7.18
/note= "Hydrophilic region"
                    ¥.
                   AAE23839 standard; peptide; 24
                                                                               Human zsig33-linker peptide #1.
                                                                                                                                                                                                                                                10-MAY-2001; 2001US-0853253.
                                                                                                                                                                                                                                                                    11-MAY-2000; 2000US-203300P.
                                                           10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                       (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                       US2002055156-A1.
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                           09-MAY-2002.
                                        AAE23839;
                                                                                                                                                                 Key
Region
RESULT 1
AAE23839
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11-MAY-2000; 2000US-0569271.
                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                 The invention relates to zaig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones.

The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression.

The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 mediate the presence of similar nucleic acids in samples, and therefore which patients may be in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the condition of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. ZSIG33-like bobt is used in gene therapy. The present sequence of the contraction of any part of the contraction of any part of the contraction of the present sequence of the contraction of the procession and the pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                             2SIG33-Like peptides and polynuclectides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; zsig33-like peptide; zs33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33-linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               and zsig33-like peptide is used in protein therapy.
is human zsig33-like peptide, zsig33-linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6..22
/note= "Hydrophilic antigenic site"
              Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 24; DB 23;
100.0%; Pred. No. 6.8e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Hydrophilic region"
              Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                           Claim 1; Page 28; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human zsig33-linker peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE15884 standard; peptide; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2001; 2001WO-US15091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
              Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                         WPI; 2002-443750/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 24; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA;
                                                        N-PSDB; AAD38239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200187933-A2.
              Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE15884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
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The invention relates to zsigi3-like peptides (2531EP) including zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsig-33-delta and zsigi3-like peptides. Zsile peptides actid molecules encoding such casigi3-like peptides. Zsile peptides actid molecules encoding such patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and solate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation of prowth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These collocations are useful for treating disorders associated with anatholate and growth related diseases. ZS31EP peptides, nucleic actids and/or antibodies are useful for treating disorders associated and contractine and actids and growth related diseases. ZS31EP peptides, nucleic actids and actids and growth related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghrelin; preproghrelin; GHS-R lb; benign prostatic hyperplasia; therapy; breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic; cancer; human.
                                                                                                                                                                                                                         nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with gastrointestinal contractility, secretion of digestive enzymes, normone and acids, secretion of hormones in the pancreas and/or brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        New polypeptides, useful for modulating gastric contractility, nu uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises zsig33-like peptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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    Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 24; DB 23; 100.0%; Pred. No. 6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
    Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human exon 3-deleted ghrelin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim la; Page 81; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
                                                                                    WPI; 2002-082982/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                 N-PSDB; AAD25760
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are concentration acid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising are an antibody specific for a peptide of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with an accompanying side effects. The present sequence represents a ghrelin type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                                New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mature protein"
                                                                                                                                               Claim 3; Page 186-187; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ALAGWLRPEDGGQAEGAEDELEVR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW87991 standard; Protein; 117 AA.
                                                                                                          of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US05620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein designated zsig33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deisher TA, Sheppard PO;
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  WPI; 2001-159704/16.
N-PSDB; AAF59647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070071/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW87991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                             breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a {\rm GHS-R}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exon-3 deleted preproghtelin and/or a GHS-H b proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghtelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choricoarcinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                         Identifying a cancer cell or tissue for treating prostate, ovarian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 24; Length 91; 100.0%; Pred. No. 2.1e-15; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosoda H, Matsuo H,
                                                                                                                                                                                                                                     Herington AC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                         (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           1b proteins or nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                 10-MAY-2002; 2002WO-AU00582
                                                                                                                           10-MAY-2001; 2001AU-0004919
17-DEC-2001; 2001AU-0009567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2000; 2000WO-JP04907
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Best Local Similarity 100.0
Matches 24; Conservative
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                                                                                                                                                                                                                                   Chopin LK, Jeffery PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kojima M,
                                                                                                                                                                                                                                                                           WPI; 2003-111957/10.
N-PSDB; AAD50726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200107475-A1.
WO200290387-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2001
                                          14-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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Gaps

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21-JAN-2000; 2000US-048B725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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                                                                                                  The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes/acids, gastrointestinal motility, recruitment of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient ebsorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satisty or treat obesity and other metabolic disorders where neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psorlasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimær's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
foung J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                   zsig33 agonists, antagonists and ligands and to produce antibodies.
                         Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                        100.0%; Score 24; DB 20; Length 1.7 100.0%; Pred. No. 2.6e-15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      52 ALAGWLRPEDGGQAEGAEDELEVR 75
                                                                                                                                                                                                                                                                                                                                                                                       1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                            Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY87236 standard; Protein; 117 AA.
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98US-0102686.
98US-0112129.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                            24; Conservative
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                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscular dystrophy
                                                                                                                                                                                                                                                                                                          117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lal P, Tang YT,
N-PSDB; AAX04550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200000610-A2.
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Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2000
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01-OCT-1998)
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                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                     Query Match
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Antional Deptide containing process with the HSPP-14. HSPPs have the Antional Deptide containing process. Antional Deptide containing process. Antional Deptide containing process. Antional Deptide containing process. And can neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation activity or function of HSPP. Such diseases include cell proliferation of HSPP are used to treat or prevent diseases include cell proliferation of HSPP are or function of HSPP. Such diseases include cell proliferation or including cancer), inflammation, cardiovascular, neurological, carthwas, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP cucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, corgenetic variations, and for chromosomal mapping. HSPP are also used to matagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic cancagonists, in competitive drug screens, and for purification of HSPP.
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                                                                                                                                                                                                                                                                                                                                                                                              AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                  New human signal peptide-containing proteins useful in treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                            prevention and diagnosis of e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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100.0%; Pred. No. 2.6e-15;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               Claim 1; Page 168-169; 327pp; English.
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                                                                                                                                                                                                                      cardiovascular disease
WPI; 2000-160673/14.
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Best Local Similarity
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                                              N-PSDB; AAZ98121
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Deisher TA, Bishop PD;

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22-NOV-2000; 2000WO-US32074.
                                                                                                99US-0166765.
                                                                                                                                                                              Jaspers SR,
                                                                                                                                       ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                      WPI; 2001-355879/37.
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                                                                                                                                                                                                                                        N-PSDB; AAF83678
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                                                                                                                                                                              Sheppard PO,
                                                                                                22-NOV-1999;
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Local Sim.
24;
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                    31-MAY-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           The Invention relates to human nucleic acids (AAIS7798-AAI61369) and the ancoded polypeptides (AAM3642-AAM42213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral socierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and incluments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-1; growth hormone; bone; gastrointestinal; glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R; G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- 'specifically claimed fragment that binds to the GHS-R"
                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                              Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 24; DB 22; Length 117; 100.0%; Pred. No. 2.6e-15; Live 0; Mismatches 0; Indels (
                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                          Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                            Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                         such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-065450.
14-SEP-2000; 2000US-0662191.
19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
2000US-0598042
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nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human zsig33 polypeptide.
                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI58046.
                                                                                                                                                                            , Liu C,
Wang Z,
                                                                                                                                                                                                                   Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200138355-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification.
                                03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                            Tang YT,
Wang J,
                                                                                                                                                                                                                 Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB62649;
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IID AAB6
XX AAC AAB6
XXX XXX XXX
XXX E3-J
XXX E4-J
XX E4-J
XX
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The invention relates to a method of forming a reversible peptidereceptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (Comprising residues 24-37 of AAB62649), where the receptor builds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and parcreatic enzymes and hormones, secretion of insulin-like growth factor. It is secretion of non-zsig33 proteins. It is useful for modulating growth cormone secretion in a mammal having a disease associated with abnormal common secretion of non-zsig33 proteins. It is useful for modulating growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, skeletal dysplasia, immune suppression, obesity, growth retardation, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety requalation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zaig33 polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
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Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
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100.0%; Pred. No. 2.6e-15;
tive 0; Mismatches 0;
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/label- Signal_peptide
24..117
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29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                Kojima M,
                                                                   WPI; 2001-159704/16.
                              (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                              N-PSDB; AAF59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1999;
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                                                Kangawa K,
                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                             The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see Secretagoque receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue, andulating pancreatic secretion of hormones and digestive enzymes, inducting growth hormone secretion, and modulating gastric emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                            Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric emptying -
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
/label- Mature_protein
24..34
/label- SGIP_peptide
/note- "this peptide is claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 24; DB 22; Length 1 100.0%; Pred. No. 2.6e-15;
                                                                                                                                               Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                               Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB60511 standard; Protein; 117 AA
                                                                                                                                                                                                                                              Disclosure; 54; 61pp; English.
                                                                                    2000WO-US18306
                                                                                                       99US-0345157
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                                                                                                                                               Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                           (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                 WPI; 2001-123010/13
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
                                                                                                                                                                           N-PSDB; AAF30033,
                                                                                                                                                                                                                           gastric emptying
                                              WO200100830-A1
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                                                                                                                                               Sheppard PO,
                                                                                    30-JUN-2000;
                                                                                                       30-JUN-1999;
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                                                                 04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
         Peptide
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one manno acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a local encompasses the unmodified peptides; the DNA encoding the peptide is also encompasses the unmodified peptides; the DNA encoding the peptides comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with the compounds of the invention are safe with the present sequence represents and an accompanying side effects. The present sequence represents a
                                                                                                                                                                                                     New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis of infant growth disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ghrelin-type growth hormone secretagogue (GHS) precursor protein
of the invention.
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Matsuo H, Minamitake Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 24; DB 22;
100.0%; Pred. No. 2.6e-15;
tive 0; Mismatches 0;
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24..119
/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 182; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB78319 standard; Protein; 117 AA
Hosoda H,
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nes 24; Conservative
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The invention relates to zaigi3-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG31 in samples (e.g. by enzyme linked immunosorbent assays (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein.
ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; zsig33-11ke peptide; ZS33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; anthypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
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/label= Signal_peptide
24..117
/note= "Human mature zsig33 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 23; 100.0%; Pred. No. 2.6e-15; Vermatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                         Disclosure; Page 27; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE15883 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000; 2000US-0569271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; zsig33 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAE15883
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                                                                                                                                                                                                                                                                                  The present sequence represents human zsig33. The specification describes a short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to motilin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by SGIP. SGIP may also be used as an antigen in the production of antibodies against SGIP and in assays to identify modulators of SGIP expression and activity. The anti-SGIP antibodies, agonists and antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies, agonists and antibodies may also be used as diagnostic agents for detecting the presence of SGIP in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; zsig33-like peptide; gastric contractility; nutrient uptake;
growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                     New Short Gastrointestinal Peptide, which has homology to motil useful for preventing, diagnosing and treating gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                              Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                              Disclosure; Columns 39-40; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 ALAGWLRPEDGGQAEGAEDELEVR 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE23838 standard; Protein; 117 AA
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                                            Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
(ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human zsig33 protein.
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N-PSDB; AAD38238.
                                                                                    WPI; 2002-634794/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                              N-PSDB; ABV72214
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AAE23838
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Gaps

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98WO-US19330.
98WO-US19437.
98WO-US21141.
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99WO-US28565
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2000WO-US04414
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2000WO-US15264
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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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11-FEB-2000;
18-FEB-2000;
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14 - SEP - 1998;
14 - SEP - 1998;
16 - SEP - 1998;
17 - SEP - 1998;
07 - OCT - 1998;
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15-SEP-1999;
15-SEP-1999;
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20-DEC-1999;
22-DEC-1999;
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02-MAR-2000;
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02-JUN-2000;
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29-OCT-1998;
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20-APR-1999;
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29-NOV-1999;
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                                               28-AUG-1998,
10-SEP-1998;
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02-DEC-1999;
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The invention relates to zsigi3-like peptides (zsigib) including zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsigi3-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsigi3-delta and zsigi3-linker, zsigi3-beta, zsigi3-gamma, zsigi3-delta and zsigi3-like peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in other developmental processes. They are useful for evaluating functions of hypothalams-pitulitary-adreal axis, to modulate containing functions of hypothalams-pitulitary-adreal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-chanancers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as containing glucose and as adsorption channers for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues associated diseases. ZS331p peptides, nucleic acids and/or antibodies are useful for treating disorders associated the more and acids and contractility, secretion of diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone and acids, secretion of hormones in the pancreas and/or brain, agastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33 protein.
                                                             New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises ssign3-like peptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 24; DB 23; Length 117; 100.0%; Pred. No. 2.6e-15; Live 0; Mismatches 0; Indels (
                                                                                                                                               Disclosure; Page 80-81; 89pp; English.
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Best Local Similarity 100.
Matches 24; Conservative
            WPI; 2002-082982/11.
N-PSDB; AAD25759.
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ABU66790
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Human; secreted protein; transmembrane protein; PRO; inflammatory disease, organ fallure, atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; blosensor; acquired immunodeficiency syndrome; cancer; diabetic complication;
                                                                                                                                                                            Human secreted/transmembrane, PRO, protein SEQ ID 442
                                          ABU67066 standard; Protein; 117 AA.
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98WO-US17888
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99WO-US30095
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05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
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14.SEP-1998;
14.SEP-1998;
14.SEP-1998;
16.SEP-1998;
07-OCT-1998;
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28-AUG-1998
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                                                                                    ABU67066;
RESULT 15
                     ABU67066
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The PRO polypeptides are useful for for stimulating the researce of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of generating transgenic animals or PRO polypeptides of the invention.

PRO polypeptides of the invention.

PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DeForge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane PRO nucleic acids, useful for gene
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100.0%; Score 24; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                          2001US-0802706.
2001US-0808689.
2001US-0816744.
2001US-0828366.
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2001US-0854280.
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Gerritsen ME, Goddard A,
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Smith V, Stewart TA,
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N-PSDB; ACA03823.
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2000WO-US04414

18-FEB-2000; 18-FEB-2000; 22-FEB-2000;

ò g under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, and the proliferation of differentiation of chondrocyte cells, the proliferation of conditional the release or proteins from cartilage, proliferation of inner ear urticular supporting cells, the proliferation of T-lymphocyte cells, the release or proliferation of endothelial cells, a method for modulating the uptake of a cytokine from peripheral blood mononclear cells (PBMC), or the proliferation of endothelial cells, a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucledic acids and any of the nucleic sequences cited above. The nucleic acids and an oligonate and any of the nucleic acids and an oligonate and an animal and an oligonate acids and an oligonate acids and an oligonate acids and an acid and an animal and an oligonate acids and an acid and an acid and an acid acids and aci

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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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N-PSDB; ACA04244.
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The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmebrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited

Claim 12; Fig 442; 659pp; English.

Gao W;

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probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,

The present sequence represents a PRO protein of the invention.

bioreactors. Both are

biosensors or

useful in tissue typing

polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation

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US-09-989-735-268
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US-09-990-52-268
US-09-990-511-268
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US-09-991-726-268
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Fatent No. US20020055156A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHEPPARD, PAUL
APPLICANT: BISHOP, PAUL
APPLICANT: BISHOP, PAUL
TILLE OF INVENTION: 2aig33-like Peptides
FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
CURRENT APPLICATION NUMBER: 60/203,300
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 4
SEQ ID NO 4
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Patent No. US20010041791A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-09-794-987-2
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C63
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR PELING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/08910
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-04-28
PRIOR PAPLICATION NUMBER: 60/084600
PRIOR PLING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
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PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                     Sequence 268, Application US/09989722 Patent No. US20020072067A1
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
                                                         24; Conservative
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Botstein, David
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Eaton, Dan L.
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                                      Similarity
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US-09-989-722-268
                Query Match
                                      Best Local
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 24; DB 9; Length 11 Similarity 100.0%; Pred. No. 3.9e-16; 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION NUMBER: 09/046,479
FILING DATE: CURROWN>
APPLICATION NUMBER: 09/046,479
FILING DATE: CURROWN>
APPLICATION NUMBER: 09/046,479
FAPLICATION NUMBER: 09/046,479
APPLICATION NUMBER: 31,438
REFERRATION NUMBER: 31,438
REFERRATION NUMBER: 37,438
REFERRATION NUMBER: 37,438
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INC. 03.03.02013.120A1.

APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, STEPHEN
APPLICANT: JASPERS, STEPHEN
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: Zaig33-like Peptides
CURRENT APPLICATION NUMBER: US/09/853,253.
CURRENT APPLICATION NUMBER: US/09/853,253.
CURRENT APPLICATION NUMBER: 06/203,300
PRIOR APPLICATION NUMBER: 60/203,300
PRIOR PILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09853253 Patent No. US20020055156Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ropology: linear
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 24; Conserva
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US-09-853-253-2
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us-09-853-253-4.oli.rapb

Gaps ö Length 117; Indels 100.0%; Score 24; DB 9; L 1larity 100.0%; Pred. No. 3.9e-16; Conservative 0; Mismatches 0; R APPLICATION NUMBER: 60/090246

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090252

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090431

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090435

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090435

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090444

R FILING DATE: 1998-06-24 REFLIENCE DATE: 1998-06-24

RAPPLICATION NUMBER: 60/090540

RAPLICATION NUMBER: 60/090540

RAPLICATION NUMBER: 60/090557

RAPLICATION NUMBER: 60/090557

REILING DATE: 1998-06-24

RAPLICATION NUMBER: 60/090676

RAPLICATION NUMBER: 60/090676

RAPLICATION NUMBER: 60/090690

RAPLICATION NUMBER: 60/090690

RAPLICATION NUMBER: 60/090690

REILING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090862

RAPLICATION NUMBER: 60/090863

REILING DATE: 1998-06-26

RAPLICATION NUMBER: 60/091478

REILING DATE: 1998-06-26

RAPLICATION NUMBER: 60/091478

REILING DATE: 1998-07-01

RAPLICATION NUMBER: 60/09154

REILING DATE: 1998-07-02

RAPLICATION NUMBER: 60/09154

REILING DATE: 1998-07-02

RAPLICATION NUMBER: 60/09153

REILING DATE: 1998-07-02

RAPLICATION NUMBER: 60/091626

RAPLICATION NUMBER: 60/091626

RAPLICATION NUMBER: 60/091626

RAPLICATION NUMBER: 60/091633

REILING DATE: 1998-07-07

RAPLICATION NUMBER: 60/091626

RAPLICATION NUMBER: 60/091626

RAPLICATION NUMBER: 60/091633

REILING DATE: 1998-07-07

RAPLICATION NUMBER: 60/091626

RAPLICAT PILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535 Similarity Query Match Best Local Simi] Matches 24; ( PRIOR PRIOR

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R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-66-04
R APPLICATION NUMBER: 60/088033
RR FILING DATE: 1998-66-04
R APPLICATION NUMBER: 60/088326
R APPLICATION NUMBER: 60/088326
R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-66-05
R FILING DATE: 1998-66-05
R FILING DATE: 1998-66-05
R FILING DATE: 1998-66-05
R APPLICATION NUMBER: 60/088212
R APPLICATION NUMBER: 60/088212
R APPLICATION NUMBER: 60/088217
R APPLICATION NUMBER: 60/088314
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DR FILING DATE: 1998-06-17
DR FILING DATE: 1998-06-18
DR APPLICATION NUMBER: 60/089901
DR APPLICATION NUMBER: 60/089907
DR APPLICATION NUMBER: 60/089908
DR FILING DATE: 1998-06-18
DR APPLICATION NUMBER: 60/089947
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089948
DR APPLICATION NUMBER: 60/089952
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R PAPLICATION NUMBER: 60/089105

R PILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16
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R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILLING DATE: 1998-06-10
FILLING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
FILLING DATE: 1998-06-10
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-10
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  FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 3001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062260
PRIOR PAPLICATION NUMBER: 60/062250
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
                                                                                                        Sequence 268, Application US/09989723 Patent. No. US20020072092A1 GENERAL INFORMATION: APPLICANT: Ashkenazi,Avi J.
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Goddard, Audrey
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                    RESULT 5
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60/088861

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APPLICANT: Shady, Camin 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same CURRENT FILE OF INVENTION: Acids Encoding the Same CURRENT FILE OF THE 1997-10-17

PRIOR PELICATION NUMBER: 60/04987

PRIOR RELIGATION NUMBER: 60/04987

PRIOR RELIGATION NUMBER: 60/06250

PRIOR PELICATION NUMBER: 60/06311

PRIOR PILICATION NUMBER: 60/08910

PRIOR PELICATION NUMBER: 60/08902

PRIOR PILICATION NUMBER: 60/08903

PRIOR PILICATION NUMBER: 60/08903

PRIOR PILICATION NUMBER: 60/08903

PRIOR PILICATION NUMBER: 60/0802

PRIOR PILICATION NUMBER: 60/0803

PRIOR PILICATION NUMBER: 60/08033

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PRIOR PILICATION NUMBER: 60/08033
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R APPLICATION NUMBER: 60/088026

R APPLICATION NUMBER: 60/088028

R APPLICATION NUMBER: 60/088028

R APPLICATION NUMBER: 60/088028

R APPLICATION NUMBER: 60/088029

R APPLICATION NUMBER: 60/088039

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
                                                                                                           Eaton, Dan L.
Ferrara, Napoleone
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Napier, Mary A.
                   Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                     Goddard, Audrey
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APPLICANT:
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Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1998 06-23
PRIOR PELING DATE: 1998 06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR PILING DATE: 1998-06-24
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PRIOR PELING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION NUMBER: 60/09163
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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US-09-989-279-268 ; Sequence 268, Application US/09989279 ? Patent No. US20020072496A1 ; GENERAL INFORMATION:

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PRIOR PAPLICATION NUMBER: 60/08912
PRIOR APPLICATION NUMBER: 60/08912
PRIOR APPLICATION NUMBER: 60/08912
PRIOR APPLICATION NUMBER: 60/08913
PRIOR APPLICATION NUMBER: 60/08913
PRIOR PLILING DATE: 1999-66-63
PRIOR PLILING DATE: 1998-66-60
PRIOR PLILING DATE: 1998-66-10
PRIOR PLILING DATE: 1998-66-11
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PRIOR PLILING DATE: 1998-66-11
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100.0%; Pred. No. 3.9e-16;
Wemarches 0;
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR PILING DATE: 1998-06-34
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; Sequence 268 Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
APPLICANT: AARhenazi,Avu J.
APPLICANT: Baker,Kevin P.
; APPLICANT: Baker,Kevin P.
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
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R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/089105

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/08912

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089513

R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089599

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R APPLICATION NUMBER: 60/090349

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R APPLICATION NUMBER: 60/088826
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R APPLICATION NUMBER: 60/088888881
R FILING DATE: 1998-06-11
R R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/088861
                                                                                                                                         R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088814
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
                                            FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
                        APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-05
                        PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT APPLICATION NUMBER: 2001-11-19
PRIOR FILING DATE: 1997-06-16
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PRIOR PILING DATE: 1999-03-20
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RELING DATE: 1998-06-02

RELING DATE: 1998-06-03

RAPLICATION NUMBER: 60/08/159

RAPLICATION NUMBER: 60/08/159

RAPLICATION NUMBER: 60/08/02

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RELING DATE: 1998-06-04

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RELING DATE: 1998-06-04
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088212
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                                                                                         Grimaldi, J. Christopher
                                                                                                                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                        Gerritsen, Mary E. Goddard, Audrey
                                                                                                                                                                                                                 Paoni, Nicholas F
  Gerber, Hanspeter
                                                                        'n.
                                                                                                                     Gurney, Austin L
                                                                                                                                              Kljavin, Ivar J
                                                                                                                                                                    Napler, Mary A.
                                                                        Sodowski, Paul
                                                                                                                                                                                               Pan, James
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APPLICANT SCHOOL AND APPLICANT SCHOOL APPLICANT SCHO
                                                                           Roy, Margaret Ann
Stewart, Timothy A.
                                                   Paoni, Nicholas F.
     Napier, Mary A.
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100.0%; Pred. No. 3.9e-16;
1ive 0; Mismatches 0; Indels
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R APPLICATION NUMBER: 60/090690

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R APPLICATION NUMBER: 60/090694

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R FILING DATE: 1998-06-25
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R FILING DATE: 1998-07-01
R PILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
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                                                                                                               APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
FILING DATE: 1998-06-24
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090472
                                              APPLICATION NUMBER: 60/090535
                                                                                               APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-07-02
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Gurney, Austin L.
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                     1998-06-24
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Godowski, Paul
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Eaton, Dan L.
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R APPLICATION NUMBER: 60/085598

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/085599

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089601

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089901

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089907

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089908

R FILING DATE: 1998-06-18

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R FILING DATE: 1998-06-18

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                                     FILING DATE: 1998-06-10
APPLICATION UNMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08861
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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FILLING DATE: 1998-06-12
APPLICATION NUMBER: 60/08940
FILLING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
APPLICATION NUMBER: 60/088742
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Gaps ö Length 117; Indels 100.0%; Score 24; DB 10; 100.0%; Pred. No. 3.9e-16; 1ive 0; Mismatches 0; PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090678
PRIOR PLING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090691
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091869
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02 1 ALAGWLRPEDGGQAEGAEDELEVR 24 PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09 Local Similarity 100. nes 24; Conservative Query Match Best Loca Matches

Sequence 268, Application US/09989732 Patent No. US20020123463A1 GENERAL INFORMATION: Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Eaton, Dan L. Ferrara, Napoleone Fong, Sherman Gerritsen, Mary E. Goddard, Audrey Gerber, Hanspeter Kljavin, Ivar J. APPLICANT: Ashkenazi, Avi J Baker, Kevin P. Botstein, David Napier, Mary A. Desnoyers, Luc US-09-989-732-268 APPLICANT:
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APPLICANT: APPLICANT: APPLICANT:

APPLICANT

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APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT PAILOR DATE: 2001-11-19

FILE REPERENCE: PAING DATE: 2001-11-19

PRIOR PELICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR PELICATION NUMBER: 60/065186

PRIOR APPLICATION NUMBER: 60/06511

PRIOR APPLICATION NUMBER: 60/06511

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-14

PRIOR FILING DATE: 1998-01-25

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/081302

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-05-07

PRIOR PRIOR FILING DATE: 1998-05-07

PRIOR FILING DATE: 1998-05-07
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R FILING DATE: 1998-66-05
R FILING DATE: 1998-66-05
R PILING DATE: 1998-66-05
R APPLICATION NUMBER: 60/088212
R APPLICATION NUMBER: 60/08652
R APPLICATION NUMBER: 60/08655
R FILING DATE: 1998-06-09
R TILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-66-10
R APPLICATION NUMBER: 60/088738
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R APPLICATION NUMBER: 60/088738
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R APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION UNMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
Williams, P. Mickey
Wood, William I.
  APPLICANT:
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PRIOR FILING DATE: 1998-06-10
PRIOR PRILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089712
PRIOR PELLING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PELLING DATE: 1998-06-17
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PRIOR PELLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-26-24
PRIOR PELLING DATE: 1998-06-26-26
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PRIOR APPLICATION NUMBER: 00/049787
PRIOR APPLICATION NUMBER: 60/065250
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-13
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PRIOR PLING DATE: 1998-00-2-25
PRIOR PLING DATE: 1998-00-2-25
PRIOR PLING DATE: 1998-00-3-20
PRIOR PPLICATION NUMBER: 60/088029
PRIOR PPLICATION NUMBER: 60/088029
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PRIOR PPLICATION NUMBER: 60/08803
PRIOR PPLICATION NUMBER: 60/088
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: A Acids Encoding the Same
FILE REFERENCE: P2730PIC15
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                    PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-26
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PRIOR PILING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091360
PRIOR PLING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/09154
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/090690
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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Napier,Mary A.
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Botstein, David
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Eaton, Dan L.
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US-09-991-073-268
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APPLICANT:
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R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R APLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R APPLICATION NUMBER: 60/089653
R APPLICATION NUMBER: 60/089801
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542
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R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
                                                                 FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
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Sequence 268, Application US/09990442 Patent No. US20020132252A1 GENERAL INFORMATION:

US-09-990-442-268

APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David

Godowski, Paul J. Grimaldi, J.Christopher Gurney, Austin L.

APPLICANT:

APPLICANT APPLICANT

Ferrara, Napoleone

Fong, Sherman

Desnoyers, Luc

Eaton, Dan L.

APPLICANT

Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: P2730PIC8 CURRENT APPLICATION NUMBER: US/09/990,442 CURRENT FILING DATE: 2001-11-14

Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel

Zhang, Zemin

APPLICANT: APPLICANT: APPLICANT:

APPLICANT

Paoni, Nicholas F.

APPLICANT

Kljavin, Ivar J. Napier, Mary A.

PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/09154
PRIOR APPLICATION NUMBER: 60/09159
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
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PRIOR FILING DATE: 1998-06-16
PRIOR PILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08538
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PRIOR PILLING DATE: 199

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A APPLICATION NUMBER: 60/083322

BR FILING DATE: 1998-04-28

BR FILING DATE: 1998-04-28

BR FILING DATE: 1998-05-07

BR APPLICATION NUMBER: 60/087106

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BR FILING DATE: 1998-06-28

BR FILING DATE: 1998-06-02

BR FILING DATE: 1998-06-02

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BR FILING DATE: 1998-06-03

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RAPPLICATION NUMBER: 60/088028

RAPPLICATION NUMBER: 60/088028

RELING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/088030

RELING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/088030

RAPPLICATION NUMBER: 60/08826

RELING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/08826

RELING DATE: 1998-06-05

RAPPLICATION NUMBER: 60/08820

RAPPLICATION NUMBER: 60/08821

RELING DATE: 1998-06-05

RAPPLICATION NUMBER: 60/08821

RELING DATE: 1998-06-05

RAPPLICATION NUMBER: 60/08831

RELING DATE: 1998-06-05

RAPPLICATION NUMBER: 60/088742

RELING DATE: 1998-06-10

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NR APPLICATION NUMBER: 60/089105

NR FILING DATE: 1998-06-12

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NR FILING DATE: 1998-06-16

NR APPLICATION NUMBER: 60/089512

NR FILING DATE: 1998-06-16

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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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                                        PRIOR REPRESENTANT OF THE PRIOR REPRESENTANT
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliam I.
APPLICANT: Annoy, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PL17
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0;
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                                                             PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PAPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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RAPELICATION NUMBER: 60/062250
RAPELICATION NUMBER: 60/065186
RELING DATE: 1997-10-17
RAPELICATION NUMBER: 60/065186
RELING DATE: 1997-11-12
RAPELICATION NUMBER: 60/065311
RELING DATE: 1997-11-24
RAPELICATION NUMBER: 60/066770
RELING DATE: 1997-11-24
RAPELICATION NUMBER: 60/075945
RELING DATE: 1998-02-25
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RELING DATE: 1998-02-25
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02
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Gerber, Hanspeter
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/09559
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PRIOR APPLICATION NUMBER: 60/09563
PRIOR APPLICATION NUMBER: 60/09961
PRIOR APPLICATION NUMBER: 60/09961
PRIOR PELLIKG DATE: 1938-66-17
PRIOR PELLIKG DATE: 1938-66-17
PRIOR PELLIKG DATE: 1938-66-19
PRIOR PELLIKG DATE: 1939-66-19
PRIOR PELLIKG DATE: 1939-66-13
PRIOR PELLIKG DATE: 1939-66-14
PRIOR PELLIKG DATE: 1939-66-15
PRIOR P
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
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100.0%; Pred. No. 3.9e-16;
Live 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR APPLICATION NUMBER: 60/092182
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; Patent No. US20020137075A1
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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nes 24; Conservative
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PRIOR FILING DATE: 1998-06-18
PRIOR PAPLICATION NUMBER: 60/089907
PRIOR APPLICATION NUMBER: 60/089408
PRIOR APPLICATION NUMBER: 60/08941
PRIOR APPLICATION NUMBER: 60/08941
PRIOR PILING DATE: 1988-06-19
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PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PILING DATE: 1998-07-07

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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088028

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088039

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088031

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088031

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088031

R FILING DATE: 1998-06-07

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R APPLICATION NUMBER: 60/088167

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088212

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R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

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R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/08876

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-12

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/08940

R FILING DATE: 1998-06-16

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R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
R APPLICATION NUMBER: 60/089601
R APPLICATION NUMBER: 60/08961
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/08824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
                                 APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-16
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/08861
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TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P7330PLC22
CURRENT APPLICATION NUMBER: US/09/990,456
FRIOR PRICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06531
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06531
PRIOR FILING DATE: 1997-11-34
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-05-26
PRIOR PLING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
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Pred. No. 3.9e-16;
                                                                      Query Match 100.0%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 3.9 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/09990456 Patent No. US20020137890A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
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Napier, Mary A.
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Eaton, Dan L.
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US-09-990-456-268
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APPLICANY: Zhang, Zemin Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic PILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic PILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same PROPE PROPERTY FILING DATE: 2001.11.19
PRIOR PELLING DATE: 1997-06.16
PRIOR PELLING DATE: 1997-01.10
PRIOR PELLING DATE: 1997-11.13
PRIOR PELLING DATE: 1997-11.13
PRIOR PELLING DATE: 1997-11.13
PRIOR PELLING DATE: 1998-01.20
PRIOR PELLING DA
                                  1 ALAGWLRPEDGGQAEGAEDELEVR 24
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US-09-989-721-268
; Sequence 268, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
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Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
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Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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100.0%; Score 24; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 24; Conservative 0; Mismatches 0;
                                               PRIOR APPLICATION NUMBER: 60/08952
PRIOR FILING DATE: 1998-06-19
PRIOR PAPLICATION NUMBER: 60/090246
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PAPLICATION NUMBER: 60/090254
PRIOR PAPLICATION NUMBER: 60/090349
PRIOR PILING DATE: 1998-06-23
PRIOR PAPLICATION NUMBER: 60/090355
PRIOR PAPLICATION NUMBER: 60/090355
PRIOR PAPLICATION NUMBER: 60/090429
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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             1998-06-19
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THE APPLICATION NUMBER: 60/088033

RAPPLICATION NUMBER: 60/088033

RAPPLICATION NUMBER: 60/088033

RAPPLICATION NUMBER: 60/088126

RELING DATE: 1998-06-04

RELING DATE: 1998-06-05

RELING DATE: 1998-06-10

RAPPLICATION NUMBER: 60/088138

RELING DATE: 1998-06-10

RAPPLICATION NUMBER: 60/08810

RELING DATE: 1998-06-10

RAPPLICATION NUMBER: 60/08810

RELING DATE: 1998-06-10

REPLICATION NUMBER: 60/088810

RELING DATE: 1998-06-10

RELING DATE: 1998-06-10 THE FILTING DATE: 1998-06 11

RAPELICATION NUMBER: 60/088861

RAPELICATION NUMBER: 60/088861

RAPELICATION NUMBER: 60/088861

RAPELICATION NUMBER: 60/089105

REILING DATE: 1998-06-11

RAPELICATION NUMBER: 60/08940

RAPELICATION NUMBER: 60/089410

RAPELICATION NUMBER: 60/089512

REILING DATE: 1998-06-16

RAPELICATION NUMBER: 60/089512

REILING DATE: 1998-06-16

REILING DATE: 1998-06-16 R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08538

R RFILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08558

R RILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08559

R APPLICATION NUMBER: 60/08559

R APPLICATION NUMBER: 60/089500

R FILING DATE: 1998-06-17 FILING DATE: 1998-06-04
APPLICATION UNDRER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030 APPLICATION NUMBER: 60/089653 FILLING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18
APPLICATION UNMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090252

PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PRILORION NUMBER: 60/09043
PRIOR PILING DATE: 1998-06-24
PRIOR PRILORION NUMBER: 60/090445
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090696
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PRIOR PAPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/091636
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/091636
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-03
PRIOR PELING DATE: 199

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Length 117;

100.0%; Score 24; DB 10; 100.0%; Pred. No. 3.9e-16; ive 0; Mismatches 0;

Query Match 100.0%; Score 24; DE Best Local Similarity 100.0%; Pred. No. 3.9 Matches 24; Conservative 0; Mismatches

Search completed: September 11, 2003, 18:16:17 Job time : 14.7594 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 11, 2003, 17:46:37; Search time 9.1123 Seconds (without alignments) 253.289 Million cell updates/sec Run on:

US-09-853-253-4 24 1 ALAGWLRPEDGGQAEGAEDELEVR 24 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283308 seqs, 96168682 residues Searched:

0 Word size :

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Descri	dhrelin precursor			c	aconitate hydratas	BOLF1 protein - hu		conserved hypothet	probable membrane	conserved hypothet	quiescence-specifi	hypothetical prote	hypothetical prote		ပ	HL-60-induced diff			C	tropomyosin I, tho	tropomyosin I, emb	PD-1 protein - hum	lipoprotein mtsA,	hypothetical prote	_	hypothetical prote	Ø		
ID	A59316	T04453	JH0572	A48990	B83451	OOBE10	C87574	F82266	AB0401	E82118	A30230	T46695	A91082	B85927	D69070	A40866	T30002	A95298	CTPGP	B25624	A25624	A55737	T48894	H83433	H71852	H72757	T35144	T48871	572509
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Length	117	483	302	344	910	1239	69	103	142	175	178	180	189	189	198	223	237	265	267	284	284	288	289	289	290	293	299	302	308
Query Match	100.0	33.3	29.5			29.5	25.0		•				25.0		25.0	25.0						•		25.0	25.0	•	25.0	25.0	25.0
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hypothetical protein F4D11.80 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C; Accession: T04453 F; Rechman, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998

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A; Molecule type: DNA
A; Residues: 1-483 <BEV>
A; Cross-references: EMBL:AL022537
A; Experimental source: cultivar Columbia; BAC clone F4D11
C; Genetics:
A; Map position: 4
A; Introns: 17/3; 44/1; 94/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2

A; Accession: T04453

conserved hypothet probable phosphogl	transcription repr 30s ribosomal prot probable prolibopr	hypothetical prote sam-dependent meth	cysteine proteinas cysteine proteinas	protein F1N19.7 {1 hypothetical prote	alcohol dehydrogen cysteine proteinas	phosphoribosylamin molybdopterin bios	hypothetical prote
E82762 F64129	E69690 AH1823 T35063	A83526 AE3323	S71923 S59598	G96668 AD2697	G97314 T47471	DCBSPK D82801	F83321
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# ALIGNMENTS

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A; Molecule type: mRNA
A; Residues: 1-117 < KOJ>
A; Cross-references: GB: AB029434; NID: 96691571; PIDN: BAA89371.1; PID: 96691572
A; Experimental source: tissue stomach endocrine cells
A; Note: submitted to GenBank, June 1999
C; Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gr
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girelin precursor - human
N;Alternate names: preproghtelin
C;Species: Homo sapiens (man)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 21-Jul-2000
C;Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product; ghrelin #status predicted <MAT>
F;22-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;25-117/Domain: carboxyl-terminal propeptide #status experimental
F;26/Binding site: octanoate (Ser) (covalent) #status experimental
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Local Similarity 100.0%; Pred. No. 3.3e-17;
hes 24; Conservative 0; Mismatches 0;
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C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C; Accession: C87574
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heftelberg,
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Telefacter Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                        GB:AE004091; NID:g9947516; PIDN:AAG04951.1; GSPDB:GN
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larblg, K.; .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
Nature 406, Asserte genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p A; Reference number: A82950; MUID:20437337; PMID:10984043
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
A;Contents: unman herpesvirus 4 BOLFI protein
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C;Superfamily: iron-responsive element-binding protein
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100.0%; Pred. No. 25;
iive 0; Mismatches
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100.0%; Pred. No. 33;
iive 0; Mismatches
                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-910 <STO>
A; Cross-references: GB:AE004584; GF
A; Experimental source: strain PAO1
C; Genetics:
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Matches 7; Conservative
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A Molecule type: DNA
A, Residues: 1-69 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                        Appointerized Figure 10. Streptomyces invitations (it.d.) incommentally concentrally streptomyces lividans (c) Species: Streptomyces lividans (c) Species: Streptomyces lividans (c) Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-1999 (c) Accession: JH652. Busse, L.A.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.; Gene 111, 125-130, 1992 (c) A.F.; Smith, G.A.; Narhi, L.O.; McGinley, M.O.; Rohde, M.F.; Gene 111, 125-130, 1992 (c) A.F.; McGene number: JH6571; MuID:92192468; PMID:1547948 (c) A.R. Accession: JH6572 (c) A.R. Accession: JH6573 (c) Accession: JH6573 (c) A.R. Accession: JH6573 (c) Accession: JH6773 (c) Accession: JH6
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C; Species: Streptomyces lividans
C; Species: Streptomyces lividans
C; Species: Streptomyces lividans
C; Species: Streptomyces lividans
C; Accession: A48990
B; Butler, M.J.; Davey, C.C.; Krygsman, P.; Walczyk, E.; Malek, L.T.
A; Title: Cloning of genetic loci involved in endoprotease activity in Streptomyces livid
A; Reference number: A48990; MUID: 93099553; PMID: 1464066
A; Accession: A48990
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-344 < GUTY>
A; Note: sequence extracted from NCBI backbone (NCBIN: 121210, NCBIP: 121213)
C; Superfamily: Pseudomonas putida regulatory protein catR
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                                                                      Length 483
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                                                   33.3%; Score 8; DB 2;
100.0%; Pred. No. 1.5;
iive 0; Mismatches
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Best Local Similarity luv...
Best Local 8; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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302 QAEGAEDE 309
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|100 ALAGWLR 106
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   A; Note: F4D11.80
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Gaps

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Cispecies: Vibrio cholerae
Cispecies: Nature 4000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cispecies: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cispecies: Nature 4000 No. 1. Ermolaeva, M.D.; Venter, J.S.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Notacule type: DNA
A;Rosidues: 1-175 <HEL>
A;Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95256.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; blotype El Tor
C;Genetics:
A;Gene: VC2111
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A; Residues: 1-178 <BED>
F; Dozin, B.; Descalz!, F.; Briata, L.; Hayashi, M.; Gentili, C.; Hayashi, K.; Quarto,
J. Biol. Chem. 267, 2979-2985, 1992
A; Title: Expression, regulation, and tissue distribution of the Ch21 protein during c
A; Reference number: A42581; MUID:92147639; PMID:1737754
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A;Title: The amino terminal sequence of the developmentally regulated CH21 protein sh A;Reference number: A35491; MUID:90267487; PMID:2346493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quiescence-specific protein precursor - chicken
N.Alternate names: Ch21 protein
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 15-Nov-1996
C;Accession: A30230; A42581; A36595; A55491
R;Bedard, P.A.; Yannoni, Y.; Simmons, D.L.; Erikson, R.L.
Mol. Cell. Biol. 9, 1371-1375, 1989
A;Title: Rapid repression of quiescence-specific gene expression by epidermal growth A;Reference number: A30230; MuID:89261749; PMID:2498647
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A; Molecule type: mRNA
A; Residues: 1-95,'L','97-178 <-DO2>
A; Residues: 1-95,'L','97-178 <-DO2>
A; Residues: 1-95,'L','97-178 <-DO2>
A; Residues: 1-95,'L','97-178 <-DO2>
A; Ricancedas: E.D.; Dozin, B.; Rosal, E.; Molina, F.; Cancedda, R.; Negri, A.; Ronchi, J. Blol. Chem. 265, 19060-19064, 1990
A; Title: The Ch21 protein, developmentally regulated in chick embryo, belongs to the A; Reference number: A36595; MUID:91035433; PMID:2229062
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100.0%; Pred. No. 67;
tive 0; Mismatches
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A;Molecule type: protein
A;Residues: 21-48 < CAS.
C;Superfamily: lipocalin; lipocalin homology
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A; Residues: 21-95,'L','97-178 <CAN>
A; Cross-references: GB:M37611
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Matches 6; Conservative
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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82266
A;Status: preliminary
A;Molecule type: DNA
A;Residuas: 1-103 <AEI>
A;Cross-references: GB:AE004173; GB:AE003852; NID:99555341; PIDN:AAF94049.1; GSPDB:GN001
C;Genetics:
A;Gene: VC0887
A;Gene: VC0887
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C; Species: Yersinia pestis
C; Date: O2N Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AB0401
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R; Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein VC0887 (imported) - Vibrio cholerae (strain N16961 serog
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A;Gene: YP03302
C;Superfamily: hypothetical protein H10489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species; Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
C;Accession: F82266
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A;Accession: AB0401
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <KUR>
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C; Superfamily: major cold shock protein; cold shock domain homology
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0.31;
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100.0%; Pred. No. 44;
tive 0; Mismatches
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C;Superfamily: uncharacterized conserved protein
                                                              Query Match 25.0%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches
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Matches 6; Conservative
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|130 EGAEDE 135
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ORF-180 [imported] - Lactobacillus helveticus plasmid pLH1 C;Species: Lactobacillus helveticus C;Species: Lactobacillus helveticus C;Species: Lactobacillus helveticus C;Species: Lactobacillus helveticus C;Species: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000 C;Accession: T46695 R;Thompson, K.; McConville, K.J.; McReynolds, C.; Foley, S. Submitted to the EMBL Data Library, December 1997 A;Description: Complete sequence of plasmid pLH1 from Lactobacillus helveticus A;Cession: T46695 A;Reference number: 223135 A;Accession: T46695 A;Accessi
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A;Experlmental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                 Gaps
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-178/Product: quiescence-specific protein #status predicted <MAT>
F;25-173/Domain: lipocalin homology <LIP>
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                                                                                                                                                                                                                          Length 178;
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100.0%; Pred. No. 68;
11ve 0; Mismatches
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Best Local Similarity 100.0
Matches 6; Conservative
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65 EDELEV 70
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31 ALAGWL 36
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|4 ALAGWL 19
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imidazoleglycerol-phosphate synthase - Methanobacterium thermoautotrophicum (strain D C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacter-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999 C; Accession: D69070 R; Smith, D.R.; Doucette-Stamm, L.A.; Delougherry, C.; Lee, H.; Dubois, J.; Aldredge, T.; Ginth, D.R.; Doucette-Stamm, L.A.; Delougherry, C.; Lee, H.; Dubois, J.; Aldredge, T.; Gintch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-198 <MTH>
A;Residues: 1-198 <MTH>
A;Cross-references: GB:AE000912; GB:AE000666; NID:92622632; PIDN:AABB5999.1; PID:9262 A;Experimental source: strain Delta H
hypothetical protein 24080 [imported] - Escherichia coli (strain O157:H7, substrain E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 189;
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A;Start codon: TTG
C;Superfamily: amidotransferase hisH; trpG homology
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100.0%; Pred. No. 72;
ative 0; Mismatches
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 11, 2003, 17:30:37; Search time 4.62032 Seconds Run on:

(without alignments) 244.278 Million cell updates/sec

US-09-853-253-4 24 1 ALAGWLRPEDGGQAEGAEDELEVR Perfect score: Sequence:

24

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	otion	homo sapien	bos taurus	streptomyce	streptomyce	epstein-bar	canis famil	qallus qall		s corticotr	drosophila	homo sapien		helicobacte					bacillus su	brucella me	zea mays (m	bacillus su					mycoplasma		bos taurus	homo sapien	hordeum vul	homo sapien	buchnera ap	candida alb
	Description	nqn6	09bd16	091127	P43161	P03189	Q9bef8	P21760	027568	P01192	P09491	015116	042431	Q9zk75	08p280	Q9a157	09pf88	P45250	P36944	Q8y174	010717	P12045	009689	Q99ti6	002554	P47491	P78022	P26638	09gmb8	P49591	P16098	012899	08k1x3	0/4261
SUMMARIES	ID	HRL	GHRL_BOVIN	MPR2_STRCO	MPRR_STRLI	V120_EBV	GHRL_CANFA	EFAB_CHICK	HIS5_METTH	COLI_PIG	TPM2_DROME	PCD1_HUMAN	OPSD_LIMPA	PARB_HELPJ	MTSA_STRP8	MTSA_STRPY	MRAW_XYLFA	YF56_HAEIN	RBSR_BACSU	MRAW_BRUME	CYS2_MAI2E	PURK_BACSU	IF5_SCHPO	TIG_STAAM	CUS1_YEAST	RPSD_MYCGE	RPSD_MYCPN	SYS_MOUSE	SYS_BOVIN	SYS_HUMAN	AMYB_HORVU	Z173_HUMAN	CH60_BUCTC	HS60_CANAL
	DB		-	-		-	-	-	7	-	-	-	-	7	_	-	-	7	-	-	٦	-	-	-	-	-	-	-	-			-1	٦,	4
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	Result No.	1	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50	30	31	32	33

	Q92154 coturnix co P26242 rhodobacter P51693 homo sapien			070141 rattus norv P25516 escherichia
HS60_YEAST HS60_AJECA	SMP_COTJA DXS_RHOCA APP1_HUMAN	HUTH_MOUSE 2263_HUMAN HELS AFROF	UVRC_STRCO SM6B_MOUSE	SM6B_RAT ACO1_ECOLI
пП				
572	620 641 650	657 683 702	728	887 890
25.0	25.0 25.0 25.0	25.0	25.0	25.0
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34 35	36 37 38	39 400 1	1 4 4 1 5 E	44 45

# ALIGNMENTS

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TISSUE-Blood,

WEDLINE-22388257; PubMed-12477932;

REDLINE-22388257; PubMed-12477932;

Strausberg R.L., Feingold E.A., Gerus. C.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Toshiyuki S., Carninof P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Wuzny D.M., Soderignes B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mylting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Schmutz J., Mysers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Mysers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20067959; Pubmed-10604470;
Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          GHRL_HUMAN STANDARD; PRT; 117 AA.
QQUBU3: QGTAT9; Q9H3R3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomesetto C., "Karam S.M., Rio M.-C.; "Identification of a novel gastric protein m46."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kojima M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
Wajnrajch M.P., Ten I.S., Gerriner J.M., Leibel R.L.;
"Genomic corganization of the human Ghreiin gene.";
J. Endocrinol. Genet. 1:231-233(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                      GHRL OR MTLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kojima M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stomach
                                       GHRL_HUMAN
RESULT 1
                                                                                                                      DDT TDD DT TDD D
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Gaps

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Indels

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Mismatches

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100.0%; Score 24; DB 1; Length 117; 100.0%; Pred. No. 6e-18;
117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                       llarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12792 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 24-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 QAEGAEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AA;
                                                               Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                              Query Match
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                                                                                                                                                                                                                                                          GHRL_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIPID
                                                                                                                                                                                                                                         RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold-09UBU3-1; Sequence-Displayed;
Name-2; Synonyms-del-Gln14-ghrelin;
Isold-09UBU3-1; Sequence-PVSP_003245;
PTM: O-n-octanoylation is essential for activity.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/GhraliniD327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Luropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 605353; -.

MIM; 605353; -.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0005613; E:growth hormone receptor ligand activity; TAS.

GO; GO:0007186; P:cell-cell signaling; TAS.

GO; GO:0007186; P:G-procein coupled receptor protein signalin. . .; TAS.

InterPro: IPR006737; motilin_assoc.

InterPro: IPR006738; motilin_dhrelin.

Fina: PF04643; motilin_assoc; 1.

Pfam: PF04644; motilin_assoc; 1.

Pfam: PF04644; motilin_assoc; 1.
                                                                                                                                                                                                                                                                                                                                                                               Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                   MEDLINE-21203998; PubMed-11306336; Kojima M., Hosoda H., Matsuo H., Kangawa K.; Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
                                                                                                                                                                  Tomasetto C., Karam S.M., Ribleras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motillin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMOVED IN MATURE FORM.
N-OCTANOATE.
Missing (in isoform 2).
/FIIGHVSP_003245.
L -> M (IN REF. 5).
                                           and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                           TISSUE-Stomach;
MEDLINE-20389976; Pubmed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB029434; BAA89371.1; --
EMBL, AJ25278; CAB6573.1; --
EMBL, AF296558; AAG10300.1; --
EMBL, AF296558; AAG10300.1; --
FMBL, BC025791; AAH25791.1; --
PIR; A59316; A59316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth regulation.
                                                                                                         SEQUENCE OF 24-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                  REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
  RRARE REPRESENTATION OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kojima M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type I (GHSR) inducing the release of growth hormone from
the pituitary. Has an appetite-stimulating effect, induces
addposity and stimulates gastric acid secretion. Involved in
growth regulation (By similarity).

-- SUBCELLULAR LOCATION: Secreted (By similarity).
-- SUBCELLULAR LOCATION: Secreted (By similarity).
-- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR006738; motilin_ghrelin.
InterPro; IPR00541; Preproghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04644; motilin_ghrelin.
Pf04644; motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
PRINTS; PR01624; GHRELIN.
HOTDOM; PD332162; Preproghrelin; 1.
HOTMOND; Cleavage on pair of basic residues; Signal; Lipoprotein.
SIGNAL.
                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 1; Length 116
Pred. No. 0.0014;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY S
N-OCTANOATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> E (IN REF. 2).
F55536DAC5FA59B6 CRC64;
       116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006737; motilin_assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%; Scor.
100.0%; Pre
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GHRL_BOVIN STANDARD;
Q9BDJ6; Q9GKY6;
28-FEB-2003 (Rel. 41, Created)
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MPR2_STRCO

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                                                                                                                                                                                                                                                                                                                                                                      MEDINE-92192468; PubMed=1547948; Lichenstein H.S., Busse L.A., Smith G.A., Narhl L.O., McGinley M.O., Rohde M.F., Katzowitz J.L., Zukowski M.M.; "Cloning and characterization of a gene encoding extracellular metalloprotease from Streptomyces lividans."; Gene 111:125-130(1992).
                                                                                                                                                                                                                                           Streptomyces lividans 66: a novel neutral protease gene with an adjacent divergent putative regulatory gene.";

Can. J. Microbiol. 38:912-920(1992).
                                                                                                                                                                                                           Butler M.J., Davey C.C., Krygsman P., Walczyk E., Malek L.T., "Cloning of genetic loci involved in endoprotease activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M894/b; AMARCOVIII, LYSR_B.
InterPor; IPR000347; HTH_LYSR.
InterPror; IPR00119; LySR_Subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF003466; LySR_Substrate; 1.
Pfam; PF003466; LySR_Substrate; 1.
Transcription regulation; DNA-binding; Activator.
DNA_BIND 20 39 H-T-H MOTIF (POTENTIAL).
CONFILCT 270 270 G -> AR (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
lo. 4.4;
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21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ....
  Small neutral protease regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gammaherpesvirinae; Lymphocryptovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M81703; AAA26739.1; -.
EMBL; M89476; AAA26804.1; ALT_INIT.
                                                                                                                                                                      STRAIN-66 / 1326;
MEDLINE-93099553; PubMed-1464066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capsid assembly protein BOLF1. BOLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMALL NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-305 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                     Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||
| 104 ALAGWLR 110
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                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                    NCBI_TaxID-1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATORS.
                                                                                                                                                                                                                                                                                                                                                           STRAIN-TK24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V120_EBV
P03189;
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  а
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Gendeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Protease; Transcription regulation; Complete proteome.
DNA_BIND 20
SEQUENCE 328 AA; 35885 MW; 2BA97730AE4FA16B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces NCBI_TaxID=1902;
                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1;
Pred. No. 4.3;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                        328 AA
                                                                                                                                                                                                                            Small neutral protease regulatory protein. MPRR OR MPRR2 OR SCO7433 OR SC6D11.29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL939131; CAB76352.1; -.
InterPro; IPR000847; HTH_LysR.
InterPro; IPR005119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00126; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                        STANDARD;
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104 ALAGWLR 110
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les 7; Conserv
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28-FEB-2003
                                                                                                                   MPR2_STRCO
Q9L127;
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P43161;
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MPRR_STRLI

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RESULT 4

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   or send an
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                 Name=1; Synonyms=Chrelin;
IsoId=09BEF8-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=09BEF8-2; Sequence=VSP_003244;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                 Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Glbson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomasetto C., Wendling C., Rio M.-C., Poitras P.; "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHRL_CANFA STANDARD; PRT; 117 AA.

G9BEF8; 09BEF7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
G6relln precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1239;
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1239 AA; 132748 MW; 6C5DBFC55F2FF729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 7; DB 1;
100.0%; Pred. No. 13;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth regulation (By similarity).
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). TISSUE-Gastric fundus;
 MEDLINE-84270667; PubMed-6087149;
                                                                                                                                                                                                                                                                                                                          EMBL; V01555; CAA24841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                             PIR; A43041; QQBE10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 696 AEGAEDE 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                           Capsid assembl
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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MEDLINE-89261749; PubMed-2498647;
Bedard P.-A., Yannoni Y., Simmons D.L., Erikson R.L.;
Rapid repression of quiescence-specific gene expression by epidermal growth factor, insulin, and pp60v-src.";
Mol. Cell. Biol. 9:1371-1375(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giannonl P., Dozin B., Zambotti A., Neri M., Cancedda R.; "Differentiation-dependent activation of the extracellular fatty acid binding protein (EXFABP) gene in chicken embryo chondrocytes."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-178 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-91035433; PubMed-2229062;
Cancedda F.D., Dozin B., Rossi F., Molina F., Cancedda R.,
Negri A., Ronchi S.;
"The Ch21 protein, developmentally regulated in chick embryo, belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression, regulation, and tissue distribution of the Ch21 protein and furing chicken embryonenes:".
                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                       basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P21760; P21928; Q9PWN9; Created)
01-MAY-1991 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Extracellular fatty acid binding protein precursor (Ex-FABP)
(Quiescence-specific protein) (P20K) (Ch21 protein).
                                                                                                                                                                                                                               BY SIMILARITY.
GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIM
N-OCTANOATE (BY SIMILARITY).
MISSING (in 1soform 2).
/FTIG-VSP_003244.
W; 3ES7FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92147639; Pubmed-1737754;
Dozin B., Descalzi F., Briata L., Hayashi M., Gentili C.,
Hayashi K., Quarto R., Cancedda R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 19;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AA
                                   InterPro: IPR006738; motilin_assoc.
InterPro: IPR006738; motilin_ghrelin.
InterPro: IPR006738; motilin_ghrelin.
Pfam; PP04644; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic resi
                                                                                                                                                                                                                                                                                                                                                                                                       Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ring chicken embryogenesis.";
Biol. Chem. 267:2979-2985(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
EMBL; AJ298295; CAC29155.1; -. EMBL; AJ298296; CAC29156.1; -.
                                                                                                                                                                                                                                                                                                                                                              117 AA; 13007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                     25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                             Alternative splicing
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 AEDELE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: PREFERENTIALLY SYNTHESIZED IN NONPROLIFERATING
                                                                                                                                                                                                                                                                                                                                                                                                        Descalzi Cancedda F., Dozin B., Zerega B., Cermelli S., Cancedda R.;
"Ex-FABP: a fatty acid binding lipocalin developmentally regulated in chicken endochondral bone formation and myogenesis.";
Biochim. Biophys. Acta 1482.127-135(2000).
-!- FUNCTION: Preferentially binds long-chain unsaturated fatty acids such as linoleic acid, oleic acid, arachidonic acid. Also binds with a lower affinity long chain saturated fatty acids such as steraic acid. May act as survival protein by playing a role in maintaining cell viability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR FATTY ACID BINDING PROTEIN.
                                                                                                        protein shows homology with amino terminal sequences of low molecular weight proteins binding hydrophobic molecules."; Blochem. Blophys. Res. Commun. 168:933-938(1990).
                                 SEQUENCE OF 21-48.
MEDLINE-90267487; PubMed-2346493;
Cancedda F.D., Asaro D., Molina F., Cancedda R., Caruso C.,
Camardella L., Negri A., Ronchl S.;
"The amino terminal sequence of the developmentally regulated Ch21
                                                                                                                                                                      STRAIN-White leghorn; TISSUE-Bone marrow;
MEDLINE-92195690; PubMed-1549365;
Nakano T.;
Graf T.;
Ildentification of genes differentially expressed in two types of v-myb-transformed avian myelomonocytic cells.";
the superfamily of lipophilic molecule carrier proteins.";
Biol. Chem. 265:19060-19064(1990).

    MISCELLANEOUS: Developmentally regulated in chick embryo.
    SIMILARITY: Belongs to the lipocalin family.

                                                                                                                                                                                                                                                                                                 Cancedda F.D., Malpell M., Gentili C., Di Marzo V., Bet P., Carlevaro M., Cermelli S., Cancedda R.; The developmentally regulated avian Ch21 lipocalin is an extracellular fatty acid-binding protein."; J. Biol. Chem. 271:20163-20169(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

L -> S (IN REF. 2).

R -> S (IN REF. 2 AND 4).

F -> S (IN REF. 2 AND 4).
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InterPro; IPR000566; Lipocin_cytFABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61199; -; NOT_ANNOTATED_CDS.
PIR; A30230; A30230.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20513977; PubMed-11058755;
                                                                                                                                                                                                                                                                                     MEDLINE-96355330; PubMed-8702740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                           SEQUENCE OF 103-178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipocalin; Transport;
SIGNAL 1 20
                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anticope T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Adredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Adredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Adredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Anticope T., Ragie P., Meng Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
Amologali S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine
amidotransferase activity that produces the ammonia necessary to
hisF for the synthesis of IGP and AICAR (By similarity).
C. -!- CATALYTIC ACTIVITY: 5-[(5-phosphor-1-deoxyribulos-1-carboxamide + L-glutamine - inidazole-glycerol phosphate + 5-
aminoinidazol-ylatamine - inidazole-glycerol phosphate + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Histidine biosynthesis; fifth step. SUBUNIT: Heterodimer of hisH and hisF (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hish (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hish) (IMGP synthase subunit hish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0442; GATASE_TYPE_1; 1.
Histidine biosynthesis; Transferase; Glutamine amidotransferase;
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                    Score 6; DB 1; Length 178;
Pred. No. 27;
                                                                                                                                                                              Indels
F -> S (IN REF. 1).
L -> V (IN REF. 1).
ODDBDC33C1AOC6B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AA.
                                                                                                                                      100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacteriaceae; Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY
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                                                          20201 MW;
                                                                                                                    25.0%;
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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62
96
178 AA;
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6; Conserv
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027568;
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                                                          SEQUENCE
                                                                                                                       Query Match
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MEDLINE-74306590; Pubmed-4369114;
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    REAL BREEF B
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MEDLINE-95046835; PubMed-7958386;
Gen K., Hiral T., Kato T., Kato Y.;
Fresence of the same transcript of pro-opiomelanocortin (POMC) genes in the porcine anterior and intermediate pituitary lobes.";
Mol. Cell. Endocrinol. 103:101-108(1994).
                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-04.239607; PubMed-6547437;
Oates E., Herbert E.;
"5' sequence of porcine and rat pro-opiomelanocortin mRNA. One and two rat forms.";
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Gossard F.J., Chang A.C.Y., Cohen S.N.;
"Sequence of the cDNA encoding porcine pro-opiomelanocortin.";
Blochim. Blophys. Acta 866:68-74(1986).
                                                                Length 198
                                                                                                          Indels
                   E8EFA43EC9163AEF CRC64;
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Riniker B., Sieber P., Rittel W., Zuber H.;
Revised amino-acid sequences for porcine and human
adrenocarticatrophia hormone ".
                                                                                                                                                                                                                                                                                                COLI_PIG STANDARD; PRT; 267 AA. P01122; Q95246; 21-JUL-1986 (Rel. 01, Created) 23-CT-1986 (Rel. 02, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                              DB 1;
                                                           25.0%; Score 6; DB 1
100.0%; Pred. No. 29;
:ive 0; Mismatches
  BY SIMILARITY
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Nature New Biol. 235:114-115(1972).
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                   21348 MW;
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                                                                                                          6; Conservative
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Eukaryota; Metazoa;
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                                                                                                                                                                                            EGAEDE 135
                   198 AA;
                                                                                      Best Local Similarity
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ACT_SITE
SEQUENCE
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                                                              Query Match
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Voigt K., Stegmaler W., McGregor G.P., Roesch H., Seliger H.;
"Isolation and full structural characterisation of six
adrenocorticotropin-like peptides from porcine pituitary gland.
Identification of three novel fragments of adrenocorticotropin and of
two forms of a novel adrenocorticotropin-like peptide.";
Eur. J. Biochem. 194:225-236(1990).
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MEDLINE=76100762: PubMed=1207728;
Hughes J., Smith T.W., Kosterlitz H.W., Fothergill L.A., Morgan B.A.,
Morris H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris J.L., Lerner A.B.; "Amino-acid sequence of the alpha-melanocyte-stimulating hormone."; Nature 179:1346-1347(1957).
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Graf L., Barat E., Patthy A.;
"Isolation of a COOH-terminal beta-lipotropin fragment (residues
61-91) with morphine-like analgesic activity from porcine pituitary
glands.";
"Re-examination of the sequence of the C-terminal tryptic fragment from porcine adrenocorticotropic hormone."; Acta Biochim. Biophys. Acad. Sci. Hung. 7:293-297(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (In) Melenhofer J. (eds.);
Chemistry and biology of peptides, pp.609-611, Ann Arbor Sci. Pub.
Ann Arbor (1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gilardeau C., Chretien M.;
"Complete amino acid sequence of porcine beta-lipotropic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of two related pentapeptides from the brain with potent opiate agonist activity."; Nature 258:577-579(1975).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pankov Y.A., Yudaev N.A.; "Complete amino acid sequence in the molecule of porcine beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 217-234.
Harris J.I., Roos P.;
"Amino-acid sequence of a melanophore-stimulating peptide.";
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Geschwind II., Li C.H., Barnafi L.;
Tructure of the beta-melanocyte-stimulating hormone.";
J. Am. Chem. Soc. 79:620-625(1957).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graf L., Barat E., Cseh G., Sajgo M.;
"Amino acid sequence of porcine beta-lipotropic hormone.";
Biochim. Biophys. Acta 229:276-278(1971).
                                                                                                                                                                            MEDLINE-91071194; PubMed-2174774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 136-148.
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of the D. melanogaster third chromosome."; Cell 37:469-481(1984).
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                                                                          melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                    AMIDATION (G-149 PROVIDE AMIDE GROUP).

N-LINKED (GLCNAC. . .) (POTENTIAL).

G >> S (IN REF. 3 AND 4).

T -> A (IN REF. 3 AND 4).

G -> E (IN REF. 3 AND 4).

G -> E (IN REF. 4).

A -> S (IN REF. 4).
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MEDLINE-84205681; PubMed-6202423;
Karlik C.C., Mahaffey J.W., Coutu M.D., Fyrberg E.A.;
"Organization of contractile protein genes within the 88F subdivision
         -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD THE DIFFERENT ACTIVE PEPTIDES.
-1- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                                                                               INTERMEDIARY PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                         PRINTS; PR00383; MELANOCORTIN.
Endorphin; Hormone; Cleavage on pair of basic residues; Amidation;
                                                                                                                                                                                                                                                                                                                                                MET-ENKEPHALIN.
AMIDATION (G-88 PROVIDE AMIDE GROUP).
AMIDATION (G-149 PROVIDE AMIDE GROUP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NGBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                              MELANOTROPIN GAMMA. CORTICOTROPIN.
                                                                                                                                                                                                                                                                                   MELANOTROPIN ALPHA. CORTICOTROPIN-LIKE
                                                                                                                                                                                                                                                                                                                 LIPOTROPIN GAMMA.
MELANOTROPIN BETA.
BETA-ENDORPHIN.
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Pred. No
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100.0%;
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                                                                                                                                   EMBL; X03561; CAA27248.1; -. EMBL; X00135; CAA24968.1; -. EMBL; S73519; AAB32312.1; -.
                                                                                                                                                                  EMBL; K01879; AAA31104.1; -. PIR; A93496; CTPGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                               Glycoprotein; Signal
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Best Local Similarity
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MOD_RES
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RAM Addams N.D., Celniker S.E., Li P.W., Hoshins R.A., Gocayne J.D., RA Addams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Addams N.D., Celniker S.E., Holf R.A., Bashburner M. Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Raders S. Ashburner M. Henderson S.N., Briton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Raders S. Champe M., Pfelifer B.D., Raderon G.G., Mortman J.R., Tandell M.D., Chelson C.R., Miklos G.L.G., Manti J.F., Agbayani A., An H.-J., Andrews-Pfannokoh C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basus A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Butler H., Cadlew E., Center A., Chandra I., Radrews P. Burtis R.C., Busam D.A., Buller H., Cadlew E., Center A., Chandra I., Radrews D., Belcher A., Dablike C., Davenport L.B., Davies P., A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Radrems M., Cabilista C.C., Ferraz C., Ferr
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B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; "A Drosophila full-length cDNA resource.";
SEQUENCE FROM N.A. (ISOFORMS EMBRYONIC AND THORACIC). MEDLINE=86085920; PubMad=3079761; Basi G.S., Storti R.V.; V.Y.; Storti R.V.; Stor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencort B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                              lanogaster.";
Biol. Chem. 261:817-827(1986).
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LADEMDSTFAELAGY (in isoform Embryonic).
/FIId=VSP_006616.
M -> V (IN REF. 1).
Q -> L (IN REF. 1).
I -> T (IN REF. 1).
I -> T (IN REF. 1).
A -> D (IN REF. 1).
A -> D (IN REF. 1).
AW: 07AD03FDD304EA5F CRC64;
                                                                                                                     MEDLINE-85215579; Pubmed-4000944;
Boardman M., Basi G.S., Storti R.V.;
"Multiple polyadenylation sites in a Drosophila tropomyosin gene are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Embryonic; Synonyme-129, A, B, e; Isold-P09491-2; Sequence-VSP_006616; DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEYEN-RESIDUES PERIODICITY. SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY. CAUTION: Ref. 6 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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PROSITE; PS00326; TROPOMYOSIN; 1.
Muscle protein; Colled coll; Repeat; Alternative splicing; Multigene family.
VARSPLC 259 284 RLFNEKEKYKAICDDLDOTFAELTGY ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 284;
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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                               SEQUENCE OF 258-284 FROM N.A. (ISOFORM EMBRYONIC).
                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Name=Thoracic; Synonyms=127, t;
IsoId=P09491-1; Sequence=Displayed;
                                                                                                                                                                                                                                          used to generate functional mRNAs.";
Nucleic Acids Res. 13:1763-1776(1985).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, K02622; AAA28970.1; --
EMBL, K02623; AAA28971.1; --
EMBL, K02622; AAA28971.1; --
EMBL, K03277; AAA28973.1;
EMBL, K03277; AAA28973.1;
EMBL, A2003708; AAN13652.1; --
EMBL, AY071087; AAL48709.1; --
EMBL, AY071087; 
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InterPro; IPR000533; Tropomyosin.
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88 88 Q
95 25 I
255 255 R
284 AA; 32981 MW;
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Pfam; PF00261; Tropomyosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene model prediction.
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Best Local Similarity
Matches 6; Conserv
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PCD1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Apoptosis.
                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97473511; PubMed-9332365;
Finger L.R., Pu J., Masserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
"The human Pp-1 gene: complete.cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
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Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
Gene 203:253-253(1997).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                           [1]
SEQUENCE FROM N.A.
MEDLINE-95154844; PubMed-7851902;
Shinohara T., Taniwaki M., Ishida Y., Kawaich M., Honjo T.;
"Structure and chromosomal localization of the human PD-1 gene
                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: POSSIBLE CELL DEATH INDUCER, IN ASSOCIATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
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-!- DEVELOPMENTAL STAGE: INDUCED AT PROGRAMMED CELL DEATH.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
PROGRAMMED CELL DEATH PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 288;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A5210AD50C3046C7 CRC64;
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HSSP: P01607; 1REI.

Genew; HGNC: 8760; PDCD1.

MIM; 600244; --

GO: 00040871; F:signal transducer activity; TAS.

GO: GO: 0006915; P:apoptosis; TAS.

GO: GO: 0007275; P:development; TAS.

GO: GO: 0007275; P:development; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003066; Ig_MHC.

FMART; SM00406; IG_V.

FMART; SM00406; IG_V.

PROSITE: P550835; IG_LIKE; 1.
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-> S (IN REF
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0; Mismatches
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88 AA;
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                                                                                                                                                                                                                                                                                                                                                   OTHER FACTORS
                           NCBI_TaxID-9606;
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CARBOHYD
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2 LAGWLR 7
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16-OCT-2001
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16-OCT-2001
                                                                                                                                                                                                            PARB_HELPJ
 DOMAIN
DISULFID
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                                 CARBOHYD
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SEQUENCE
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                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial settles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                            LINKED TO CIS-RETINAL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
VISION IN DIM LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                         -i- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED (BY SIMILARITY).
-i- SIMILARIYY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                               deduced from nuclear DNA evidence.";
Mol. Phylogenet. Evol. 8:415-422(1997).
-1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
                                                                                                                                                                                  Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Abyssocottidae; Limnocottus.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                      "Molecular evolution of the cottoid fish endemic to Lake Baikal
                                                                                                                                                                                                                                                    MEDLINE-98086781; Pubmed-9417898;
Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J., Bowmaker J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro: IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
PRNTS; PR000237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00238; OPSIN; 1.
                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                             289 AA.
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                                                                              PRT;
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                                                                             STANDARD;
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                                                                                                                                       Rhodopsin (Fragment).
                                                                                                                                                           Limnocottus pallidus
                     277 LRPEDG 282
6 LRPEDG 11
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=61634;
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                                                     RESULT 12
OPSD_LIMPA
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-i- SIMILARITY: BELONGS TO THE PARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Unid B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                Gaps
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Bacteria: Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence comparison of two unrelated isolates of the human
                                                  CHROMOPHORE (BY SIMILARITY).
                                                                            .) (POTENTIAL)
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                                                                                                                                                                         Length 289
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                                                                                                                            32715 MW; 160D08E17E5E1280 CRC64;
CYTOPLASMIC (POTENTIAL).
                                                                          N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable chromosome partitioning protein parB
                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 AA.
                                                                                                                                                                                                   41;
                                                                                                                                                                         25.0%; Score 6; DB 1
100.0%; Pred. No. 41;
iive 0; Mismatches
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                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                  RETINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001534; AAD06646.1; -. PIR; H71852; H71852. InterPro: IPR004437; ParB_part. InterPro; IPR0043115; ParBc.
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SMART; SM00470; ParB; 1
281 >5
81
267
171
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289 AA;
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245 AEDELE 250
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Best Local Similarity
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NCBI_TaxID-1314, 198466;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-21927593; Pubmed-11917108;
Smoot J.C., Barbian K.D., Wind Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Rapur V., Daly J.A., Veasy L.G., Musser J.M.,
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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09A157; 09RNJ7; 09RNJ0;
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation procursor.
MCAL ABC transporter substrate-binding lipoprotein precursor.
MTSA OR SPY0453 OR SPS1539.
Streptococcus pyogenes, and
Streptococcus pyogenes (serotype M3).
                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Metal ABC transporter substrate-binding lipoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL ABC TRANSPORTER SUBSTRATE-BINDING LIPOPROTEIN.
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InterPro; IPR006128; Lipoprotein_4.
InterPro; IPR006128; Lipoprotein_4.
InterPro; IPR006127; SBP_bac_9.
PRINTS; PR00690; ABHESNFAMILY.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Transport; Zinc transport; Iron transport; Copper; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-ACYL DIGLYCERIDE (PROBABLE).
40F613659AAD1768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 310;
                                                                                                                                                                                                                            Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                             310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 43;
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                             PRT;
                                                                                28-FEB-2003 (Rel. 41, Created)
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310 AA; 34330 MW;
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100.0%;
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                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein; Signal;
SIGNAL 1
                                                                                                                                                                                               MTSA OR SPYM18_0494
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Best Local Similarity
Matches 6: Conserv
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EDGGQA 99
                                                                                                                                                                                                                                                                                                                NCBI_TaxID-186103;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                     Streptococcus
                          STRP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                       MTSA
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MTSA_STRPY
MTSA_STRP8
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SER3O / ATCC 700294 / Serotype M1;
MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
Perretti J.J., McShan W.M., Ajdto D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roee B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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"The genome of Invasive Streptococcus pyogenes; a comparative analysis of S. pyogenes SSI-1, SF370 and MGASB322.",
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Part of an ATP-driven transport system for a metal; this protein has affinity for Zn(II), Fe(III) and Cu(II).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
-!- SIMILARITY: Belongs to the bacterial solute-binding protein family 9. Lipoprotein receptor antigen (Lrai) subfamily.
SEQUENCE FROM N.A., SEQUENCE OF 30-39, AND CHARACTERIZATION.
STRAIN-SF370 / ATCC 700294 / Serotype M1, and AP1 / Serotype M1;
MEDLINE-20032372: PubMed-10564501.
Janulczyk R., Pallon J., Bjoerck L.;
"Identification and characterization of a Streptococcus pyogenes ABC transporter with multiple specificity for metal cations.";
Microbiol. 34:596-606(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MGAS315 / Serotype M3;
MEDLINE-22133808; Pubmed-12122206;
MEDLINE-22133808; Pubmed-12122206;
MEDRES S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genôme sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
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InterPro; IPR006128; Lipoprotein_4.
InterPro; IPR006128; Lipoprotein_4.
InterPro; IPR006127; SBP_bac_9.
PRIMYS; PR00690; ADHESNFAMILY.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Transport; Zinc transport; Iron transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING LIPOPROTEIN.
N-ACYL DIGLYCERIDE (PROBABLE).
V -> A (IN STRAIN API).
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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EMBL; AF180521; AAD56939.1; -.
EMBL; AE006505; AAK33468.1; -.
EMBL; AE014143; AAM78925.1; ALT_INIT.
EMBL; AP005145; BAC64634.1; ALT_INIT.
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FT CONFLICT 26 26 T -> A (IN REF. 1).

FT CONFLICT 44 44 A -> E (IN REF. 1).

FT CONFLICT 49 50 AI -> VM (IN REF. 1).

FT CONFLICT 49 50 AI -> VM (IN REF. 1).

SQ SEQUENCE 310 AA; 34358 MW; B0F829EFIC72CADC CRC64;

QUERY MAtch 25.0%; Score 6; DB 1; Length 310;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 EDGGOA 14

Db 94 EDGGOA 99

Search Completed: September 11, 2003, 17:52:40

JOb time: 6.62032 secs
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Q26847 trypanosoma
Q897n5 bifidobacte
Q65548 bovine herp
Q43180 homo sapien
Q8jfy6 litoria cae
Q8n8h9 homo sapien
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Q9rd30 streptomyce
Q8abul yersinia pe
Q2562 onchocerca
Q8wt59 onchocerca
Q8wt56 litomosoide
Q8wt57 onchocerca
Q8w57 saccharomyc
Q8n94 homo sapien
Q9lwy4 oryza sativ
Q9lwy4 oryza sativ
Q8m7 methanosarc
Q9m7 methanosarc
Q8xxy6 ralstonia s
Q8xxy6 ralstonia s
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025791; AAH25791.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR06738; motilin_assoc; prefam; PF04643; motilin_assoc; l.
Pfam; PF04644; motilin_assoc; l.
SEQUENCE 117 AA; 12929 MW; 25B0572EBECB7610 CRC64;
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01-MAR-2003 (TrEMBLrel. 23,
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O8zzrl pyrobaculum
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269.586 Million cell updates/sec
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                                                                                                                                                             September 11, 2003, 17:46:02; Search time 22.9733 Seconds
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
A Onders C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
A Kosenam E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
A Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.;
Full Length cDNA of gene AT4932720 (GI:7270219).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AY056237, AAL07086.1: -
R InterPro; IPR006344; Lupus_La.
R InterPro; IPR006630; Lupus_La.
R InterPro; IPR006630; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AT4G32720.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                   Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF442491; AAO06965.1; -.
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                         Ghrelin preproprotein.
Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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100.0%; Pred. No. 0.00082;
tive 0; Mismatches 0; Indels
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48095 MW; E58EBAF51C35A8F7 CRC64;
   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative RNA-binding protein LAHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Matches 8; Conservative
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287 QAEGAEDE 294
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es 11; Conserva
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                            Meriones.
NCBI_TaxID=10047;
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Matches
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Q8L7E4
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SOUTHWICK A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Chall C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Chall R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY136302, AAM96968.1;

EMBL, BT000396; AAN15715.1;
                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-A0G-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 54.1 kDa protein.
F4D11.80 OR AT4G32720.
F4D11.80 OR AT4G32720.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Benes V., Rechmann S., Borkova D., Ansorge W., Hohelsel J., Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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433 AA; 48126 MW; CFFF611A29AA0318 CRC64;
                              Last sequence update)
Last annotation update)
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100.0%; Pred. No. 3.3;
tive 0; Mismatches
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                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
     Created)
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Interpro; IPR006530; Lupus_La_dom.
Interpro; IPR006504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
  ol-ocr-2002 (TrEMBLrel. 22, 01-ocr-2002 (TrEMBLrel. 22, 01-mar-2003 (TrEMBLrel. 23, uncettin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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(TrEMBLrel.
                                                                                    Hypothetical protein.
AT4G32720.
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nes 8; Conserv
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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SEQUENCE 43
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Streptomyces
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  Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C. H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsen E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barreil B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                  33.3%; Score 8; DB 10; Length 483; 100.0%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                          0; Indels
                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL022537; CAA18589-1; --
EMBL; AL161582; CAB79899.1; -.
                                                                                                                                                                                             SMANT; SWSSOLO2; RRW; 1.
Hypothetical protein.
SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:141-147(2002).
EMBL, AL939114; CAB87228.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 10639 MW; 9316F1F38C1BD492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           091063;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC02791.
                                                                                                                                                                                                                                                                                                                                                                                   103 AA.
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0; Mismatches
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MEDLINE=21996410; PubMed=12000953;
                                                                                                               InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                              PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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hes 7; Conservative
                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                    Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                              302 QAEGAEDE 309
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nes 8; Conserv
 SEQUENCE FROM N.A.
                                                         SEQUENCE FROM N.A.
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RESULT 7

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Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin 2.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                         Desanti C.L., Strohl W.R.;
Characterization of the Streptomyces sp. strain C5 snp locus and "Characterization of the Streptomyces sp. strain C5 snp locus and development of an snp-derived expression vector family.";
Submitted (DEC_2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE016748; AA004949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY072041; AAL61992.1; -.
InterPro; IPR00047; HTH_LysR.
InterPro; IPR05119; LysR_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00126; HTH_LYSR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSTTE; PS00044; HTH_LYSR_FAMILY; 1.
DNA-binding; Transcription; Transcription; Regulation.
SEQUENCE 313 AA; 34258 MW; C907C8AF5IC3FA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 AA; 48732 MW; FF2490AD097F437D CRC64;
                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trigger factor.
                                                                                                                                                                                           Streptomycineae; Streptomycetaceae; Streptomyces NCBI_TaxID=45212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 7; DB 2;
100.0%; Pred. No. 27;
iive 0; Mismatches
    313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
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100.0%; Pred. No. 35;
iive 0; Mismatches
Q8VP52 PRELIMINARY; PRT; 313 P
Q8VP52;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence
01-OCT-2002 (TrEMBLrel. 22, Last annotation
LysR-like transcriptional activator SnpR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 ALAGWLR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 DGGQAEG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 DGGQAEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAGWLR 7
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          REGULATORS.
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Q8XY49
ID Q8XY
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Gaps

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29.2%; Score 7; DB 16; Length 910; 100.0%; Pred. No. 68; 0; Indels ive 0; Mismatches 0; Indels

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910 AA; 99147 MW; C65F23CDB6FA0E1C CRC64;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                     65 ALAGWLR 71
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                           1 ALAGWLR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Complete proteome. SEQUENCE 910 AA;
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Q9V5J0
                                                                                                                                                Matches
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-2043137; Pubmed-10984043;
MEDLINE-2043137; Pubmed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brodt K.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Tenard C., Cunnac S., Demange N., Sapin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415.497-502(2022).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Probable phage-related tail transmembrane protein.
RSC1914 OR RS03483.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 887; . 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  887 AA; 94105 MW; 9A8840E5362E740E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.2%; Score 7; DB 1
100.0%; Pred. No. 67;
tive 0; Mismatches
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Pfam; PF00694; Aconitase_C; 1.
PRINTS; PR00415; ACONITASE.
ProDom; PD00511; Aconitase_N; 1.
TIGREAMS; TIGR01341; aconitase_1; 1.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_1; 1.
                              Created)
                                                                                                                                                                                                                                                                                                                                                      STRAIN-GMI1000;
MEDLINE-21681879; PubMed-11823852;
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InterPro; IPR000573; Aconitase_C.
InterPro; IPR001030; Aconitase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004584; AAG04951.1; -.
HSSP; P20004; 1ACO.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                          Ralstoniaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.2
Best Local Similarity 100.
Matches 7; Conservative
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ACNA OR PA1562.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 887 AA;
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Q913F5
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RAMENTRE-20190005; DUDMOG-1073132;

RA Adams M.D., Celniker S.E., I. P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., I. P.W., Hoskins R.A., Galle R.F.,

RA Adams A.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutcon G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutcon G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutcon G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bardon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Beeson K.Y., Beance P.V., Berman B.P., Bhandari D., Bolahakov S.,

Borkova D., Botchan M.R., Boulther H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bultler H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bultler H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bultler H., Caddeu E., Center A., Chandra I.,

RA Bodson K., Doup LE., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Bodson K., Doup LE., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Bodson K., Canjer A., Den H. R., S., Calbart W.M., Glasser K.,

R. Glodek A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Classer K.,

RA Hostin D., Houston K.A., Havland T.J., Weil M.-H., Ibegwam C.,

Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Relean H.,

RA Merkulov G., Milshina N.V., Li J., Li J., Liang Y., Lin Z.,

Liux V., Matteri B., Worfnech T.C., McLeadou M.P., Purl V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sulv B.C.,

Millams S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,

K. Hangen D.W., Worthey R., Woode T., Wolly S., Zhao Q., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
                    030550;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG18408 protein.
REXIN OR CG3451 OR CG18408 OR CG18409.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
PRT; 2376 AA
                                                                                                                                                                                                                                                                                                                                         STRAIN-Berkeley;
MEDLINE-20196006; Pubmed-10731132;
  PRELIMINARY;
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SEQUENCE
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Q9A542;
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"Drosophila Roxin, a Novel SH3 Adaptor Protein of Axin and Arrow that
Is Essential for Living in Late Stage Embryo.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., Mornosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome. T. Sequencing of Drosophila melanogaster genome. The Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Gibbs R.A.; Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 5; Length 2376;
Pred. No. 1.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2376 AA; 267666 MW; A5F2D0589B8B695C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003830; AMF58016.2; -. Flybase, FBGN0033504; rexin.
InterPro; IPRO0145.2; SH3.
PRINTS; PRO0452; SH3DOMAIN.
PRO000066, SH3; 3.
SMART; SM00355; SH3; 3.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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REXIN OR RXN OR CG3451 OR CG18408 OR CG18409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Preu. ...
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00326; SH3; 3
PROSITE; PS50002; SH3;
SEQUENCE 2376 AA; 2(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 OAEGAED 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAEGAED 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamazaki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 21173698; PubMed-11259647;

MIDLINE-21173698; PubMed-11259647;

A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Rolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

- '- SIMILARITY: BELONS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

R MBL; AE009930; AAK24591.1; -.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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SEQUENCE 69 AA; 7450 MW; 8EA80BE9EE56853C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus.
Bacteria, Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacteraceae; NCBI_TaxID=155892;
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                                                                                                                                                                                                                                                                       2376 AA; 267657 MW; 9C7BD6C7A705C888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
cold-shock domain family protein.
                                                                                                                                                                                                                                                                                                 DB 5; Lens.
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AA.
                                                                                                                                                                                                                                                                                                                  29.2%; Score 7; DB 5
100.0%; Pred. No. 1.6
iive 0; Mismatches
-i- SIMILARITY: CONTAINS 3 SH3 DOMAINS. EMBL, AB053478; BAB62017.1; -. F1YBase; FBGN0033504; rexin. InterPro; IPR002965; P_rich_extensn. InterPro; IPR001452; SH3. Pf00018; SH3; 3.
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ProDom; PD000621; Cold_shock; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002059; Cold_shock. 
Pfam; PF00313; CSD; 1.
                                                                                                                                              PRINTS; PRO1217; PRICHEXTENSN.
ProDom, PD000066; SH3; 3.
SMART; SM00326; SH3; 3.
PROSITE; PSS0002; SH3; 3.
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Best Local Similarity luv...
7; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     13 QAEGAED 19
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                                                                                                                                                                                                                                                 SH3 domain.
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MEDLINE-94336252; PubMed-8058358;
Trenbolme R.R., Tree T.I., Gillespie A.J., Guderian R., Maizels R.M.,
Bradley J.E.;
"Heterrogeneity of IgG antibody responses to cloned Onchocerca volvulus
antigens in microfiladermia positive individuals from Esmeraldas
Province, Ecuador.";
EMBL: $71371; AAC6510.2;
NON_TER
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Broc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA, 9492 MW; 22091651845CADDI CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Antigen maltose binding protein (Fragment).
Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                              Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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                             01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE0124.
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STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
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Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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45 ALAGWL 50
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OM protein - protein search, using sw model

September 11, 2003, 17:21:03 ; Search time 16.893 Seconds
(without alignments)
325.703 Million cell updates/sec Run on:

US-09-853-253-2

Title:

1 MPSPGTVCSLLLLGMLWLDL......LGKFLQDILWEEAKEAPADK 117 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	pti	HUMAN Q9ubu3 homo sapien	Q9edx0 mus n				_	018811			046617	P01307		P19971	022582	061078		09hc57	Q9z1j2		062820		091907	Q8zbk0	09ku37	Q12799 homo	Ognite	P97445 mus n					Q16653	
SUMM	ID	Α,	GHRL_MOUSE	GHRL_RAT	GHRL_CANFA	GHRL_PIG	GHRL_BOVIN	MOTI_MACMU	MOTI_HUMAN	MOTI_CAVPO	MOTI_HORSE	MOTI_PIG	MOTI_SHEEP	TYPH_HUMAN	H2B_GOSHI	TOP2_LEICH	MOTI_FELCA	WFD1_HUMAN	NEK4_MOUSE	CCAA_RABIT	MOTI_BOVIN	MOTI_RABIT	GBX2_XENLA	CUEO_YERPE	NAGZ_VIBCH	TC10_HUMAN	BA2A_HUMAN	CCAA_MOUSE	CCAA_RAT	PT1_LACLA	PT1_LACLC	PT1_STRBO	MOG_HUMAN	0000
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STA3_HUMAN STA3_MOUSE	STA3_RAT RELN_RAT	TRUA_PYRHO TAL1 KLULA	FLHA_SALTY	RS15_HALMA	HN3B_RAT	SAP_RAT	SYFB_HAEIN	CPXU_RHISN
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770	3462	333	692	155	458	554	795	447
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99	99 99	65.5	65.5	65	65	65	65	64.5
34 35	36 37	38 30	40	41	42	43	44	4.5

# ALIGNMENTS

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Crausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A both of M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Botheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Nilalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Nilalon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Niling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
MEDLINE-20067959; Pubmed-1-006440;
Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                  09UBU3; QBPAT9; Q9H3R3;
28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (Mt6 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomasetto C., Karam S.M., Rio M.-C.;
"Identification of a novel gastric protein m46.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L.;
"Genomic organization of the human Ghrelin gene.";
J. Endocrinol. Genet. 1:231-233(2000).
                                       117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                       PRT;
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SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:656-660(1999).
                                       STANDARD;
                                                                                                                                                                                                           Homo sapiens (Human).
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                                       GHRL_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                    stomach
RESULT
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Gaps

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Length 117; Indels

100.0%; Score 611; DB 1; 100.0%; Pred. No. 2.1e-54; ive 0; Mismatches 0;

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117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
                                                                                                                             Conservative
                                                                                              Local Similarity
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                                                                                                                          Matches 117;
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      SEQUENCE
                                                                     Query Match
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Name=1; Synonyms-Ghrelin;

IsoId=09UB0J-1; Sequence=Displayed;

Name=2; Synonyms-del-Gln14-ghrelin;

IsoId=09UB0J-2; Sequence=VSP_003245;

FIN: O-n-octanoylation is essential for activity.

STMILARITY: BELONGS TO THE MOTILIN FAMILY.

DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;

WWW="http://www.infoblogen.fr/services/chromcancer/Genes/GhrelinID327.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0005131; F:growth hormone receptor ligand activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro; IPR006731; motilin_assoc.
InterPro; IPR00541; Preproghrelin.
Pfam; PF04644; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21203998; PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                            Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform 2).
/FTId=VSP_003245.
L -> M (IN REF. 5).
                                                           and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM N-OCTANOATE.
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                                                                                                                                                                                                               MEDLINE-20389976; PubMed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB029434; BAA89371.1; --
EMBL; AB015700; BAB19045.1; --
EMBL; AL252278; CAB65733.1; --
EMBL; AF26658; AAG10300.1; --
EMBL; BC025791; AAH25791.1; --
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PRINTS; PR01624; GHRELIN
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51
117
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MIM; 605353; -
                                                                                                                                                   SEQUENCE OF 24-33.
                                                                                                                                                                                      TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
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A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Alzawa T., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R., Ashiburner M., Batalov S., Casavant T., Saito R., Matsuda H., Ashiburner M., Batalov S., Casavant T., Reischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Reochiwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ashibar J., Mombaerts P., Norone P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Wilming L., Washima J., Wanshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
SEQUENCE FROM N.A. (ISOFORM 1).
Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
6hrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mouse mRNA for preproghrelin."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20389976; PubMed-10930375;
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
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stomach
                                                          Rattus
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                      DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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N-OCTANDATE (BY SIMILARITY).
Missing (in isoform 2).
FFTG-VSP_003346.
EACB49DZE3CA7203 CRC64;
       Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                 Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 GO, GO:0005737; G:cytoplasm; IDA.
GO; GO:0005737; G:cytoplasm; IDA.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                SUBCELLULĂR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
MEDLINE-21203998; PubMed-11306336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                        EMBL, AB033701; BAB19046.1; -
EMBL, AB060078; BAB69857.1; -
EMBL, AK008658; BAB25814.1; -
EMBL, AK008860; BAB25934.1; -
                                                                                                                                                                                                                                                                   EMBL; AJ243503; CAB46500.1; -.
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                                                                                                          Name=1; Synonyms=Ghrelin;
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                                                                         growth regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21433488; PubMed-11549267;
Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Structure-activity relationship of ghrelin: pharmacological study of ghrelin peptides.";
Biochem. Biophys. Res. Commun. 287:142-146(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hosoda H., Kojlma M., Matsuo H., Kangawa K.; "Purification and characterization of rat des-Gln14-ghrelin, a second endogenous ligand for the growth hormone secretagogue receptor."; J. Biol. Chem. 275:21995-22000(2000).
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TISSUE SPECIFICITY: Broadly expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, intestine and adipose tissue.
PTM: O-n-octanoylation is essential for activity. The replacement of Ser-26 by aromatic tryptophan preserves ghrelin activity.
MASS SPECTROMETRY: MW-3314.9; MW_ERR-0.7; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASS SPECTROMETRY: MW-3187.1; MW_ERR-0.6; METHOD-Electrospray;
090XH7; Q9ET69;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa
"Girelini is a growth-hormone-releasing acylated peptide from
etomach".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 279:909-913(2000).
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Name=2; Synonyms=del-Gln14-ghrelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Stomach; MEDLINE-20067959; Pubmed-10604470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley, TISSUE-Stomach, MEDLINE-20357315; PubMed-10801861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULĂR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-11162448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in qastrointestinal tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND ACYLATION OF SER-26.
                                                                                                                                                                                                                                                                                                        norvegicus (Rat)
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1624; GHRELIN.
PRODOM; P1331262; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE-Gastric fundus;
Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
"Identification of cDNA encoding WTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09BEF8; Q9BEF7;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
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82.9%; Pred. No. 4.2e-45;
ive 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 2).
/FTId=VSP_003248.
8857546FE51A7691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM. N-OCTANOATE.
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Name=1; Synonyms-Ghrelin;
IsoId=Q9BEF8-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA
                                                                                                                                                                                                                                                                     PIR; BS9316; BS9316.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
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                                                                                                                                                                                                                      EMBL; AB029433; BAA89370.1; -. EMBL; AB035699; BAB11956.1; -.
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les 97; Conserv
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PROPEP
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GHRL_CANFA
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               IsoId=09BEFB-2; Sequence=VSP_003244;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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REMOVED IN MATURE FORM (BY SIMILARITY).
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone the pitulatry. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01624; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
Sus.
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15-SEB-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
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Missing (in isoform 2).
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3E57FED9D1847CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.7e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
Name-2; Synonyms-del-Gln14-ghrelin;
                                                                                                                                                                                                                                                                                                              Interpro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; preproghrelin.
Pfam; PF04643; motilin_assoc; I.
Pfam; PF04644; motilin_ghrelin; I.
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                                                                                                                                                                                                                                                                        EMBL; AJ298295; CAC29155.1; -. EMBL; AJ298296; CAC29156.1; -.
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Q9GKY5, Q9BDG8, Q9GKY4;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA; 13007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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52
26
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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PROPEP
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MOTI_MACMU 018811;
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PROPEP
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    SO THE FEET WAR BY SO THE SO T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPSPGTVCSLLLLGMLWL-DLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRP
                                    Event-Alternative splicing; Named isoforms=2;
Name-1; Synonyms-Ghrelin;
IsoId-QG6KX5-1; Sequence-Displayed;
Name-2; Synonyms-del-Ginl4-ghrelin;
IsoId-QG6KX5-2; Sequence-VSP_003247;
IsoId-QG6KX5-2; Sequence-VSP_003247;
-:- PTM: O-n-octanoylation is essential for activity (By similarity).
-:- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-OCTANOATE (BY SIMILARITY).
Missing (in isoform 2).
/FTIG-VSP_003247.
L -> P (IN REF. 2; AAK30002).
K -> E (IN REF. 2; AAK30002).
W, 856D3EID6DABIA76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 472.5; DB 1; Length
Pred. No. 1.5e-40;
8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Kita K., Harada K., Yokota H.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AR035704; BAB19049.1; -.
EMBL, AF308930; AAK19243.1; -.
EMBL, AY028942; AAK30002.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD332162; Preproghrelin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 K
12785 MW;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB035703; BAB19048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.38;
78.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHRELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
72
118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHRL_BOVIN
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PROPEP
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
NOCTANODIE (BY SIMILARITY).
K -> E (IN REF. 2).
F55536DAC5FA59B6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
SIGNAL BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Motilin precursor (Contains: Motilin; Motilin associated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 417.5; DB 1; Pred. No. 4.8e-35; 16; Mismatches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
PRINTS; PR01624; GHRELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98433861; PubMed=9762897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GH
116 RE
26 N-
34 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF350329; AAK18612.1; -. EMBL; AB035702; BAB19047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.3%;
69.2%;
[2]
SEQUENCE OF 24-99 FROM N.A.
Kojima M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Yano H., Seino Y., Fujita J., Yamada Y., Inagaki N., Takeda J.,
Bell G.I., Eddy R.L., Fan Y.-S., Byers M.G., Shows T.B., Imura H.;
"Exon-intron organization, expression, and chromosomal localization of the human motilin gene.";
FEBS Lett. 249:248-252(1989).
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MEDIINE-88030048; PubWed-3666144;
Seino Y., Tanaka K., Takeda J., Takahashi H., Mitani T., Kurono M.,
Kayano T., Koh G., Fukumoto H., Yano H., Fujita J., Inagaki N.,
Yamada Y., Imura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence of an intestinal cDNA encoding human motilin precursor."; FEBS Lett. 223:74-76(1987).
                    S Lett. 435:149-152(1998).
FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Motilin precursor (Contains: Motilin; Motilin associated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 92; DB 1; Length 115; 27.0%; Pred. No. 0.018; tive 23; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOTMONOE; Cleavage on pair of basic residues; Signal.
SIGNAL 1 25 BY SIMILARITY.
SEPTIDE 26 47 MOTILIN ASSOCIATED PEPTIDE.
SEQUENCE 115 AA; 12821 MW, FB67E1080E989159 CRC64:
                                                                                                                                                    SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 IGMRMNSROLEKYRAALEGLLSEMLPQHA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR006737; motilin_assoc.
InterPro: IPR006738; motilin_ghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF0464; motilin_ghrelin; 1.
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   monkey brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTI_HUMAN
P12872;
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                                  FEBS
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Matches
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SEQUENCE FROM N.A.

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60; 60:0005625; P:cell-cell signaling; TAS.
G0; 60:0007267; P:cell-cell signaling; TAS.
G0; 60:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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                                                                                                                            MEDLINE-89121385; Pubmed-2914635; Dea D., Bolleau G., Poltras P., Lahaie R.G.; Dea D., Bolleau G., Poltras P., Lahaie R.G.; Dea D., Bolleau G., Poltras P., Lahaie R.G.; Poltras R.G.
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InterPro; irruco, ...

Pfam; PF04643; motilin_assoc; 1.

Pfam; PF04644; motilin_ghrelin; 1.

Hormone; Cleavage on pair of basic residues; Signal; 3D-structure.
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50 115 MOTILIN ASSOCIATED PEPTIDE.
115 AA: 12920 MW; 30D4BB59B2F42783 CRC64;
                          Daikh D.I., Douglass J.O., Adelman J.P.; "Structure and expression of the human motilin gene."; DNA 8:615-621(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 88.5; DB 1
25.4%; Pred. No. 0.041;
tive 29; Mismatches 4
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EMBL; X15395; CAA33448.1; --
EMBL; X15395; CAA33448.1; JOINED.
EMBL; X15394; CAA33448.1; JOINED.
EMBL; X15394; CAA33448.1; JOINED.
EMBL; X15394; CAA68690.1; --
EMBL; M30278; AA59860.1; --
EMBL; M30278; AA59860.1; JOINED.
EMBL; M30279; AAA59860.1; JOINED.
PIR; A33323; A33323.
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MEDLINE=90091748; PubMed=2574660;
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099MP5;
28-FEB-2003 (Rel. 41, Created)
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MOTI_CAVPO
ID MOTI_CA
AC 099MP5;
DT 28-FEB-
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Local Similarity 28.9
nes 24; Conservative
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P01307;
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             NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions also as its content is no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                           TISSUE-Intestine;
MEDLINE-21099894; PubMed-11172801;
Xu L., Depoortere I., Tang M., Peeters T.L.;
"Identification and expression of the motilin precursor in the guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Present in the gut mucosa with the exception of the gastric corpus. Also present in medulla oblongata, nucleus of the solitary tract, hypophysis, spinal cord, hypothalamus, and cerebellum but not in the cerebral cortex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                           Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Perissodactyla; Equidae; Equus.
   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Motilin precursor (Contains: Motilin; Motilin associated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Motilin precursor (Contains: Motilin; Motilin associated peptide
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14.2%; Score 86.5; DB 1; Length 127;
Best Local Similarity 27.6%; Pred. No. 0.072;
Matches 32; Conservative 23; Mismatches 44; Indels 1.
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Pfam; PF04644; motilin_ghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal SIGNAL 1.
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MOTILIN ASSOCIATED
A46E90C0E7EFC220
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Interpro; IPR006737; motilin_assoc.
Interpro; IPR006738; motilin_ghrelin.
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FEBS Lett. 490:7-10(2001)
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28-FEB-2003 (Rel. 28-FEB-2003 (Rel.
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AC 046617;
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DF 80-FEB-2003
DF (MAP)] (FragGN MIN.
CS EUKARYOLS; MOCO EUKARYOLS; MOCO MAMMANILS; MAMMANILS; MAMMANILS; MOCO MAMMANILS; MO
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                                                                     Huang Z., Depoortere I., De Clercq P., Peeters T.; "Sequence and characterization of cDNA encoding the motilin precursor from chicken, dog, cow and horse. Evidence of mosaic evolution in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 FLSPEHQRVQ--QRKESKKPPAKLQPRA-LAGWLRPEDGGQAEGAEDELEVRFNAPFDVG
                                                                                                                                                                              prepromotilin.";
Gene 240:217-226(1999)
-1- FUNCTION: PLASTS AN IMPORTANT ROLE IN THE REGULATION OF
INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
01-ANG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Motilin precursor [Contains: Motilin; Motilin associated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88288231; PubMed-2456453;
Bond C.T., Nilaver G., Godfrey B., Zimmerman E.A., Adelman J.P.;
"Characterization of complementary deoxyribonucleic acid for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOTILIN.
MOTILIN ASSOCIATED PEPTIDE.
99DBCA503EAFE4C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 86; DB 1; 28.9%; Pred. No. 0.057; tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_dhrelin.
Pfam: PF04643; motilin_assoc; 1.
Pfam: PF04644; motilin_dhrelin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
TISSUE-Duodenal mucosa;
MEDLINE-20033565; PubMed-10564829;
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TYPH_HUMAN
                                                                                           MOTI_SHEEP
                                                                        RESULT 12
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-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHMIC CONTRACTION OF DODOBNAL AND COLONIC SMOOTH MUSCLE.
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90344797; PubMed-2383556;
Khan N., Graslund A., Ehrenberg A., Shriver J.;
"Sequence-specific 1H NMR assignments and secondary structure of
           "Motilin, a gastric motor activity stimulating polypeptide: the complete amino acid sequence."; Can. J. Biochem. 51:533-537(1973).
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                                                                                                                        Schubert H., Brown J.C.; "Correction to the amino acid sequence of porcine motilin."; Can. J. Biochem. 52:7-8(1974).
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MOTILIN ASSOCIATED PEPTIDE.
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6E31A1038E142671 CRC64;
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Pfan; PF04644; motilin_ghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal.
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25.0%; Pred. No. 0.19;
tive 19; Mismatches
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                                                                                                                                                                                                                   lima H., Kai Y., Kawatani H.;
Chem. Soc. Chem. Commun. 159-160(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A40932; MSPG.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
Brown J.C., Cook M.A., Dryburgh J.R.
                                                                                                                                                                                                                                                                                          MEDLINE-72043589; PubMed-4941085;
                                                                                                        MEDLINE-74138109; PubMed-4856583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  porcine motilin.";
Biochemistry 29:5743-5751(1990)
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50 119 MC
29 29 I
119 AA; 13296 MW;
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                                                                                                                                                                                                                       Yajima H.,
                                                                                                                                                                                                    SYNTHESIS.
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                                                                                         REVISION
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98087436; PubMed-9427564;

De Clercq P., Depoortere I., Peeters T.L.;
Isolation and sequencing of the cDNA encoding the motilin precursor from sheep intestine.";
Gene 202:187-191(1997).
-!- FUNCTION: FLAXE AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Gaps
                                                                                                                                                                                                         Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MOLILLIN precursor [Contains: Motilin; Motilin associated peptide
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InterPro: IPR006738; motilin_ghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal.
SIGNAL
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SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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  115 AA
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Pred. No. 1.
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  PRT;
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25.0%;
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                                                                                                                                                                                                                                                                                  Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
  STANDARD;
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TISSUE=Intestine;
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MOTI_SHEEP
018845;
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Best Local S:
Matches 21;
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Finnis C., Goodey A.R., Courtney M., Sleep D.; "Expression of recombinant platelet-derived growth factor in the yeast
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                                                                                                                                                                                                                                                                                                                                                                                               Ishikawa F., Miyazono K., Hellman U., Drexler H., Wernstedt C., Hagiwara K., Usuki K., Takaku F., Risau W., Heldin C.-H.; "Identification of anglogenic activity and the cloning and expression of platelet-derived endothelial cell growth factor."; Nature 338:557-562(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 149-244 FROM N.A., AND SEQUENCE OF 125-178 AND 236-244. MEDLINE-92236753; PubMed-1570012; Furukawa T., Yoshimura A., Sumizawa T., Haraguchi M., Akiyama S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Thymidine + phosphate - thymine + 2-deoxy-D-
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Asal K., Nakanishi K., Isobe I., Eksioglu Y.Z., Hirano A., Hama K.,
Miyamoto T., Kato T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribose 1-phosphate.
PATHWAY: Nucleotide and deoxyribonucleotide catabolism.
SUBUNIT: Homodimer.
DISEASE: DEFECTS IN ECCE1 ARE THE CAUSE OF MITOCHONDRIAL
NEUROGASTROINTESTINAL ENCEPHALOMYOPATHY (MNGIE) (ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Neurotrophic action of gliostatin on cortical neurons. Identity of gliostatin and platelet-derived endothelial cell growth factor."; J. Biol. Chem. 267:20311-20316(1992).
                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usuki K., Saras J., Waltenberger J., Miyazono K., Pierce G., Thomason A., Heldin C.-H.; "Platelet-derived endothelial cell growth factor has thymidine
15-SEP-2003 (Rel. 42, Last annotation update)
Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (T
(Platelet-derived endothelial cell growth factor) (PD-ECGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Kerlavage A.R., Fuldner R.A., Phillips C.A., Ve "Complete sequence of a chromosome 22q subtelomeric BAC."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS MNGIE.
MEDLINE-99123033; PubMed-9924029;
Nishino I., Spinazzola A., Hirano M.;
"Thymidine phosphorylase gene mutations in MNGIE, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.";
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 184:1311-1316(1992).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89181955; PubMed-2467210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92272724; Pubmed-1590793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Anglogenic factor.";
Nature 356:668-668(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylase activity."
      15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE.
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            rissue-Placenta;
                                                                                            Gliostatin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHS---QALGKFLQDILWEEA-KEAP 114
                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:000161; F:platelet-derived growth factor receptor lig. . .; TAS. GO; GO:0009132; F:thymidine phosphorylase activity; TAS. GO; GO:0000002; P:thymidine phosphorylase activity; TAS. GO; GO:0000002; P:mitochondrial genome maintenance; TAS. GO; GO:0000022; P:mitochondrial genome maintenance; TAS. GO; GO:0006220; P:pyrimidine nucleotide metabolism; TAS. InterPro; IPR000312; Glyco_trans_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECESSIVE HUMAN DISEASE ASSOCIATED WITH MULTIPLE DELETIONS OF SKELETAL MUSCLE MITOCHONRIAL DNA (MTDNA). IT IS CLINICALLY CHARACTERIZED BY ONSET BETWEEN THE SECOND AND FIFTH DECADES OF LIFE, PTOSIS, PROGRESSIVE EXTENAL OPHTHALMOPLEGIA, GASTROINTESTINAL DYSMOTILITY (OFTEN PSEUDOOBSTRUCTION), DIFFUSE LIBENCENCEPHALOPATHY, THIN BODY HABITUS, PERIPHERAL NEUROPATHY, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSPGTVCSLLLLGMLWLDLAMAGSSFL---SPEHQRVQQRKESKKPPAKLQPRALAGWLR
                                                                                                                                                                   WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=219".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: = - : - : = : = :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                    SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
MYONEUROGASTROINTESTINAL ENCEPHALOMYOPATHY); AN AUTOSOMAL
                                                                                                                                    PHOSPHORYLASES FAMILY.
DATABASE: NAME-R&D Systems' cytokine mini-reviews: ECGF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02885; Glycos_trans_3N; I.
Pfam; PF02885; Glycos_trans_3N; I.
PIRSF00015; Glycos_trans_3; I.
ProDom; PD001864; Glyco_trans_3; I.
ProDom; PD005916; Thymid_phosphls; I.
PROSITE; PS00647; THYMID_PHOSPHOSE, I.
PROSITE; PS00647; THYMID_PHOSPHOSE, I.
Anglogenesis; Repeat; Polymorphism; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 1; Length 482; 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0652FA132C3BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R-V-A-A-A-L-X(5,6)-L-G-R.
R-V-A-A-A-L-X(5,6)-L-G-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN MNGIE).
/FTId-VAR_007647.
L -> S (IN dbSNP:11479).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K -> R (IN MNGIE).
/FTId=VAR_007645.
E -> A (IN MNGIE).
/FTId=VAR_007646.
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G -> S (IN MNGIE).
/FTIG-VAR_007644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYMIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA; 49981 MW;
                                                                                                                                                                                                                                                                                                                    EMBL; M63193; AAA60043.1; -. EMBL; U62117; AAB03344.2; -. PIR; S03904; S03904. HSSP; P77836; IBRW. Genew; HGNC:3148; ECGF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%;
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Best Local Similarity 24...
Best Conservative
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342
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265
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VARIANT
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Search completed: September 11, 2003, 17:21:41
Job time : 18.893 secs
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60 AVVNGSAQGAQIGAML-----MAIRLRGMDLEETSVLTQALAQSGQQLEWPEAWRQQL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 MAGSSFLSPEHQRVQQRKE--SKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium hirsutum (Upland cotton).

Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Malvales; Malvaceae; Malvoldeae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Gaps
                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                             "cDNA clones encoding histone H3 and histone H2B from upland cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00357; HISTONE_H2B; 1.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
SEQUENCE 147 AA; 16087 MW; CEFD5C774E6E11F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TYKIYIFKVLKQVHPDIGIS-----SKAMGIMNSFINDIFEKLAQEA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 F-----KFLQDILWEEAKEA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.8%; Score 72; DB 1; Length 147; Best Local Similarity 25.2%; Pred. No. 2.4; Matches 28; Conservative 22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-cv. Deltapine 62; TISSUE-Etiolated cotyledon;
Turley R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the histone H2B family.
                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                   147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 37, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                      Plant Gene Register PGR97-182.
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T09722; T09722.
InterPro; IPR004822; Histone_core.
InterPro; IPR000558; Histone_H2B.
                                                                                                                                                                                                                                                                                                                                                                                            BP of DNA.
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00621; HISTONEH2B.
ProDom; PD000497; Histone_H2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF025667; AAB97163.1; -.
                                                                                                                                                                                                                                                                                                                                           (Gossyplum hirsutum L.).";
(In) Plant Gene Register P
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00125; histone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00427; H2B; 1
                                                 113 VDK 115
                         115 ADK 117
                                                                                                                                                                                                                                                              NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998
16-OCT-2001
                                                                                                                                                                                   Histone H2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOP2_LEICH
061078;
                                                                                                                  H2B_GOSHI
022582:
                                                                                                       H2B_GOSHI
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-- CAPALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-- CAPALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-- SUBUNIT: Homodimer (By similarity).
-- SUBCELLULAR LOCATION: Nuclear (By similarity).
-- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
-- SIMILARITY: Belongs to the type II topoisomerase family.
-- SIMILARITY: Belongs to the type II topoisomerase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                          Eukaryota; Eugienozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID•44271;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MHOM/BR/86/L669;
Tepe-Lansdell T., Mann B.J., Labombard M., Macdonald T., Slunt K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pearson R.D.;
"Isolation of a gene encoding a DNA topoisomerase II of Leishmania (Leishmania) chagasi.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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READER: PERONAL DNA_LUCK--

READER: SMO01742; DNA_LUCK--

READER: SMO0173; HATPRASE_C: 1.

DREADER: SMO0173; TOPOISOMERASE_II: 1.

DREADER: PSO0177; TOPOISOMERASE_II: 1.

READER: PSO0177; TOPOIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201 NKKPMSRKNNVKVSLSTRVAQXPGAQLGRLLPHVL 1235
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16-OCT-2001 (Rel. 40, Last annotation update) DNA topoisomerase II (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF051307, AAC05295.2; -. HSSP, P06786; IBGW. INTERPROJ. IPR003594 ATPbind_ATPase. InterPro; IPR001241; DNA_topoisoII. InterPro; IPR002205; DNA_topoisoIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.68;
27.48;
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                                                                                                                                                                                     Leishmania chagasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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acid sequenc zsig33 prote zsig33 prote PRO polypept

Human Amino Human Human Human Human Novel Novel

secreted and secreted/tra human secret

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AAE23838
AAE15883
ABU66790
ABU67066
ABU59871
ABU59871
                                                                                                                                                                                                 AAU10892
AAY66708
AAU12392
AAB65231
AAM40676
                                                                                                                                                                                                                                                                                                                                   AAB60516
AAB60510
AAB60521
AAB60520
AAB60523
ABP58240
                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73526
ABG15575
ABG20671
                                                                                                                                                                                                                                                                  AAE23840
AAE23841
                                                                                                                     ABU59420
ABU60555
ABU58046
ABU58977
                                                                                                                                                                          ARE33409
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                                                                                                                                                                                                                                                                                                            AAE15886
                                                                                                                                                                                       ABU13937
                                                                                                         ABU5927
  (without alignments)
152.215 Million cell updates/sec
                                                                                         September 11, 2003, 17:21:03; Search time 25.0267 Seconds
                                                                                                                                                                                                                                                                                                                                                                                               1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
7: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
8: /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
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9: /SIDSI/gcgdata/geneseqy-embl/AA1999.DAT:*
9: /SIDSI/gcgdata/geneseqy-embl/AA1999.DAT
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      1107863 seqs, 158726573 residues
                                                                                                                                                                       24
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                             US-09-853-253-4
126
1 ALAGWLRPEDGGQAEGAEDELEVR
                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_19Jun03:*
                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Scoring table:

Searched:

Database

Perfect score:

Run on:

seguence:

Membrane-bound pro Human PRO1066 (DNO) Human PRO1066 (UNO) Human 281933-11nke Human 281933-11nke Human 281933-11nke Human 281933-11nke Human CRFX protein Rat des-Gln14-ghre Rat des-Gln14-ghre Rat ghrelin prepro Porcine ghrelin pr

Bovine ghrelin pre Xenopus laevis nuc Murine APLP1. Mus

Human colon cancer Novel human diagno Novel human diagno

Orosophila melanog

Human secreted/tra
Novel human secret
Human secreted/tra
Human PRO polypept
Human secreted/tr
Human preproghrel1
Human PRO1066 poly
Human PRO polypept

## ALIGNMENTS

RESULT 1 AAE23839

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Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                                                                                  /note= "Hydrophilic region"
                                                                                                                                                                                       Location/Qualifiers 7..18
  ¥
                                                                                Human zsig33-linker peptide #1.
AAE23839 standard; peptide; 24
                                                                                                                                                                                                                                                                                                   10-MAY-2001; 2001US-0853253
                                                                                                                                                                                                                                                                                                                              2000US-203300P
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                      (JASP/) JASPERS S R.
(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                                                             US2002055156-A1
                                                                                                                                                                                                                                                                                                                            11-MAY-2000;
                                                                                                                                                                 Homo sapiens
                                                     10-SEP-2002
                                                                                                                                                                                                                                                                        09-MAY-2002
                          AAE23839;
                                                                                                                                                                                            Key
Region
               Human zsig33-linke
Human zsig33-linke
Human exon 3-delet
Human des-Gln.4-gh
Protein designated
                                                                                                                                                                                                                                                                                                                                                       Human signal pepti
Human polypeptide
Human zsig33 polyp
Zsig33 protein. H
                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Description

AAE23839 AAE15884 AAE33410 AAB60517 AAW87991 AAM38890 AAM38890 AAB62649

1000.0 1000.0 1000.0 1000.0 1000.0

126 126 126 126 126 126 126

SUMMARIES

DB

Length

Query Match

Score

Result

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                 The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digastive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and nucleic acids of the invention are used to man asig33-like peptide is used in protein therapy. The present sequence and zsig33-like peptide. Zsig33-linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                         ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; zsig33-like peptide; ZS33LP; Immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation; HIV; zsig33-linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 126; DB 23; Length 24; 100.0%; Pred. No. 5.7e-12; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Hydrophilic antigenic site"
            Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Hydrophilic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15884 standard; peptide; 24 AA.
                                                                                                                              Claim 1; Page 28; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zsig33-linker peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2001; 2001WO-US15091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
            Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 24; Conservative
                                    WPI; 2002-443750/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                 24 AA;
                                                  N-PSDB; AAD38239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200187933-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Region
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Matches
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The invention relates to zsig33-like peptides (zS312P) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and czsig33-like peptides and nucleic acid molecules encoding auch zsig33-like peptides. Zs312P peptides acid mulesurate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in mproving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines and in growth regulation in the liver, blood covessel formation of other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate covessel formation of tumour cells, as additives to anti-chypoglycaemic preparations containing glucose and as adsorption channers for oral drugs which require fast nutrient action and to channers for oral drugs which require fast nutrient action and to channers for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal and growth related diseases. ZS312P peptides, nucleic cacids and/or antibodies are useful for treating dysfunction associated with gastrointestinal contractility, secretion of digestive enzymes, hormone and acids, secretion of hormones and acids, secretion of hormone and regulation of nutrient absorption. Sequences of the invention and regulation of nutrient associated sequences of the invention and regulation of nutrient associated sequences of the invention and regulation of nutrient sequence is human zsig33-linker
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                                                                                                                                                                                                                                                                                                                                                                             nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                            New polypeptides, useful for modulating gastric contractility, nu uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                   Bishop PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                   Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human exon 3-deleted ghrelin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim la; Page 81; 89pp; English.
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11-MAY-2000; 2000US-0569271.
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                                                                                                                                                               Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                 (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zsig33-like peptides
                                                                                                                                                                                                                                                WPI; 2002-082982/11.
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one manno acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising are was and an assay and kit for detecting the peptides. The peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth commone deficiency. The compounds of the invention are safe with an accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                    New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 126; DB 22; Best Local Similarity 100.0%; Pred. No. 3.4e-11; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..23
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mature protein"
                                                                                                                   Claim 3; Page 186-187; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW87991 standard; Protein; 117 AA.
                                                                                   of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US05620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0822897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein designated zsig33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deisher TA, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24..117
/note= "
 WPI; 2001-159704/16.
N-PSDB; AAF59647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9842840-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW87991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pept1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                    breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exon-3 deleted preproghtelin and/or a GHS-H lb proteins or nucleic acids. The antibodies, exon 3-deleted form of preproghtelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choricorarcinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                  identifying a cancer cell or tissue for treating prostate, ovarian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 126; DB 24;
100.0%; Pred. No. 2.6e-11;
1ve 0; Mismatches 0;
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                                                                                                                                                                                       Herington AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                    (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB60517 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hosoda H,
                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0210002.
                                                                  10-MAY-2002; 2002WO-AU00582.
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                                                                                                 10-MAY-2001; 2001AU-0004919
17-DEC-2001; 2001AU-0009567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2000; 2000WO-JP04907
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Les 24; Conservative
                                                                                                                                                                                    Jeffery PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kojima M,
                                                                                                                                                                                                                     WPI; 2003-111957/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AA;
                                                                                                                                                                                                                                   N-PSDB; AAD50726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200107475-A1.
WO200290387-A1
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26-APR-2000;
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                                  14 - NOV - 2002
                                                                                                                                                                                    Chopin LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kangawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB60517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Matches
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Gaps

N-PSDB; AAX04550.

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The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety cor treat obesity and other metabolic disorders where neurological eleback modulates nutritional absorption. They are useful to identify zsig33 agonists, antagonists and ligands and to produce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimitorobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psorlasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorgone GA, Corley NC, Guegler KJ, Baughn MR; foung J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                   Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 126; DB 20;
100.0%; Pred. No. 3.4e-11;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 ALAGWLRPEDGGQAEGAEDELEVR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                              Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY87236 standard; Protein; 117 AA.
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98US-0102686.
98US-0112129.
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m IE, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity .v... hes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
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Akerblom IE,
Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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01-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY87236;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                       AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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100.0%; Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 168-169; 327pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALAGWLRPEDGGQAEGAEDELEVR 24
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25-APR-2000; 2000US-0552317.
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                             2000-160673/14.
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117 AA;
                                                                        N-PSDB; AAZ98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1.
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qq
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WPI; 2001-355879/37.
N-PSDB; AAF83678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zsig33 protein.
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                   31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB2010
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous injuries, parisher, and a localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosis, and SNy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed
                                                                                                                                                                                    Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zsig33; signal transduction; hormone; enzyme; neural development;
gastric contractility; nutrient uptake; digestive; pancreatic; human;
insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.37 /note- "specifically claimed fragment that binds to
                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                  Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
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                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 22;
100.0%; Pred. No. 3.4e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB62649 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the GHS-R"
                                    2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0...
                 2000US-0620312
                                                                                                2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human zsig33 polypeptide.
                                                                                                                                                                                                                                                                 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA;
                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                     N-PSDB; AAI58046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200138355-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification.
                                                         14-SEP-2000;
19-OCT-2000;
                                                                                                29-NOV-2000;
                                    03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saptens
                   19-JUL-2000;
                                                                                                                                                                                                                           Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB62649;
                                                                                                                                                                                rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
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The invention relates to a method of forming a reversible peptide-
receptor complex that involves providing an immobilized receptor, and
contacting the receptor with a zsig33 peptide (Comprising residues 24-37
of AAB66549), where the receptor binds to the zsig33 peptide. The method
is useful for purifying cells, purifying a peptide, stimulating signal
contacting in a cell expressing a receptor. It is also useful for
modulating secretion of hormones, neural development and/or utilization,
gastric contractility, nutrient uptake, secretion of digestive and
contractility, nutrient uptake, secretion of digestive and
contraction of non-zsig33 proteins. It is useful for modulating growth
contraction of non-zsig33 proteins. It is useful for modulating growth
contraction of non-zsig33 proteins. It is useful for modulating growth
contraction of non-zsig33 proteins. It is useful for modulating growth
contraction of non-zsig33 proteins, it is useful for modulating growth
contraction of non-zsig33 proteins, it is useful for modulating growth
contraction of non-zsig33 proteins, it is useful for modulating growth
contraction of non-zsig33 proteins a set repair and remodeling,
controlling, low osteoblast levels, cartilage repair and remodeling,
controlling, lucose absorption and metabolism and neuropathy-associated
gastrointestinal disorders, and stimulating glucose-induced insulin
controlled, a peptide ligand for the G-protein coupled receptor, GHS-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with 2s1g33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                              Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 22; 100.0%; Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..23
/label- Signal_peptide
24..117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 93-94; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qual1flers
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22-NOV-2000; 2000WO-US32074.
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                                                                                                                                                                                                                                                                              Sheppard PO, Jaspers SR,
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                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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us-09-853-253-4.rag

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29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                  Kojima M,
                                                                     WPI; 2001-159704/16.
                              (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                              N-PSDB; AAF59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUL-2002.
                                                  Kangawa K,
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB78319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB78319
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see secretagoque receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1. SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jedjunum tissue. SGIP, indudating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                 Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating gastric emptying .
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
         24..34
/label- SGIP_peptide
/note= "this peptide is claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                   Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 126; DB 22;
100.0%; Pred. No. 3.4e-11;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                   Deisher TA,
/label- Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB60511 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                  Disclosure; 54; 61pp; English.
                                                                                         30-JUN-2000; 2000WO-US18306.
                                                                                                            99US-0345157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2000; 2000WO-JP04907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .99JP-0210002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                   Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
                                                                                                                               (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                     WPI; 2001-123010/13.
N-PSDB; AAF30033.
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          117 AA;
                                                 WO200100830-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200107475-A1
                                                                                                           30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2001
                                                                     04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60511;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
AAB60511
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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one maino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a anoified amino acid and/or a non-amino acid has been substituted by a calso encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by centrical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with hormone deficiency. The present sequence represents a companying side effects. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117;
Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 126; DB 22; 100.0%; Pred. No. 3.4e-11;
Matsuo H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human zsig33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                                                                                                                                                                                                                                                                                                                               Claim 3; Page 182; 210pp; Japanese
Hosoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB78319 standard; Protein; 117
                                                                                                                                                                                                                                                        of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000US-0608810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24..119
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The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZsiG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZsiG33 methods are used as antigens in the production of antibodies against ZsiG33 and in assays to identify modulators of ZsiG33 expression and activity. The anti-ZsiG33 antibodies are also used as diagnostic agents for detecting the presence of ZsiG33 in samples (e.g. by enzyme linked immunosorbent assays (ELISA). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein.
2.S.IG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; zsig33-like peptide; ZS33LP; immunity; developmental process; infection; human immunodeficiency virus; vaccine; antihypoglycaemic; adsorption enhancer; gastrointestinal disease; growth related disease; inflammation; gene therapy; growth regulation; blood vessel formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Human mature zsig33 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 126; DB 23; 100.0%; Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                    Disclosure; Page 27; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE15883 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2001; 2001WO-US15091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human zsig33 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                 The present sequence represents human zsig33. The specification describes a short gastroIntestinal peptide (SGIP), which is derived from zsig33. SGIP has homology to mothlin. The SGIP peptide may be used in the prevention, diagnosis and treatment of diseases associated with imappropriate SGIP expression. For example, SGIP may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of SGIP by expressing inactive proteins or to supplement the patients own production of SGIP. SGIP may also be used as an antigen in the production of expression and activity. The anti-SGIP antibodies, agonists and anti-SGIP antibodies, agonists and anti-SGIP antibodies, agonists and anti-SGIP antibodies may also be used to regulate expression and activity. The anti-SGIP antibodies may also be used as diagnostic agents for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
                                                                                                                                                   New Short Gastrointestinal Peptide, which has homology to motilingseful for preventing, diagnosing and treating gastrointestinal
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                                            Deisher TA, Bishop PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 126; DB 23; 100.0%; Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                         Disclosure; Columns 39-40; 23pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the presence of SGIP in samples
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                                          Sheppard PO, Jaspers SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
(2YMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zsig33 protein.
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Best Local Similarity
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N-PSDB; AAD38238.
                                                                                    WPI; 2002-634794/68
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                                                                                                           N-PSDB; ABV72214
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RESULT 12

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99WO-US00106.
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11-FEB-2000;
18-FEB-2000;
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22-FEB-2000;
24-FEB-2000;
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25-MAY-2001;
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02-JUN-2000;
                                          28-AUG-1998;
10-SEP-1998;
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20-APR-1999;
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06-JAN-2000;
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20-NOV-1998;
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   The invention relates to zsigi3-like peptides (zsijip) including 234gi3-linker, zsigi3-beta, zsigi3-gamma, zsigi3-delta and 234gi3-linker, zsigi3-beta, zsigi3-gamma, zsigi3-delta and csijip peptides and nucleic acid molecules encoding such zsigi3-like peptides. Zsijip peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anticrepators for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as cessarch reagents for the expansion, differentiation, growth factor and charmone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These conteactine useful for treating dysfunction associated with canterial sortex of treating disorders associated with gastrointestinal and growth related diseases. Zsizup peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal and growth related diseases. Zsizup peptides, nucleic acids and/or antibodies are useful for treating disorders associated with gastrointestinal motility, recruitment of digestive enzymes, inflammation contractility secretion of hormone and acids, secretion of hormone and acids, secretion of hormones of the hormone are useful in gene therewer the engage of the expansion of hormone and acids, secretion of hormone and acids, secretion of hormones in the pancreas and/or antibodies are useful secundance of the hormone and acids, secretion of hormone and aci
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                                                        New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises ssig33-like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in gene therapy. The present sequence is human zsig33 protein.
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 126; DB 23; Length 117; 1 Similarity 100.0%; Pred. No. 3.4e-11; 24; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                Disclosure; Page 80-81; 89pp; English.
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             WPI; 2002-082982/11.
N-PSDB; AAD25759.
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Best Local Similarity
Matches 24; Conserva
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Human; secreted protein; transmembrane protein; PRO; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; blosensor; acquired immunodeficiency syndrome; cancer; diabetic complication; bloreactor; tumour.
                                                                                                                                                                                                       Human secreted/transmembrane, PRO, protein SEQ ID 442.
                                                    ABU67066 standard; Protein; 117 AA.
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15 - SEP - 1999;
25 - NOV - 1999;
30 - NOV - 1999;
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16 - DEC - 1999;
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36 - JAN - 2000;
66 - JAN - 2000;
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18-FEB-2000;
22-FEB-2000;
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Note: The sequence data for this patent was obtained in electronic formation and dispersed the formation and threefolds.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001US-0854280.
2001US-0860216.
2001WO-US19692.
2001WO-US20116.
2001WO-US21066.
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2000US-0747259.
2001US-0796498.
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2001US-0924419.
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Smith V, Stewart TA, Tume
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nes 24; Conservative
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N-PSDB; ACA03823.
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                  22-JUN-2001;
29-JUN-2001;
09-JUL-2001;
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25-MAY-2001;
01-JUN-2001;
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2000WO-US06319
2000WO-US06884
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02-MAR-2000;

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32-MAY-2000;

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30-MAY-2000;

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30-MAY-2000;

31-MAY-2000;

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10-MAY-2001;
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25-MAY-2001;
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Gao W; DeForge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, De Gerritsen ME, Goddard A, Smith V, Stewart TA, Tum

## WPI; 2003-331925/31. N-PSDB; ACA04244.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer

## Claim 12; Fig 442; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited

under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, and the proliferation of differentiation of chondrocyte cells, the proliferation of or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of finer car utricular proteoglycans from cartilage, proliferation of finer car utricular proteoglycans from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FPA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the proliferation of adipocyte cells, a method for detecting the properties are useful for treating inflammatory diseases, organ polypeptides are useful for treating inflammatory diseases, organ diabetic complications. The nucleic acids are useful a shybridisation. ö probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a PRO protein of the invention. Gaps ö 100.0%; Score 126; DB 24; Length 117; 100.0%; Pred. No. 3.4e-11; Indels Mismatches 52 ALAGWLRPEDGGQAEGAEDELEVR 75 1 ALAGWLRPEDGGQAEGAEDELEVR 24 ö 24; Conservative Similarity 117 AA; Sequence Query Match Local Best Loca Matches ò g

Search completed: September 11, 2003, 17:25:02 Job time: 25.0267 secs

Sequence 4, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32302, A Sequence 12, Appli Sequence 12, Appli Sequence 9, Appli Sequence 9, Appli Sequence 24838, A Sequence 27419, A Sequence 27419, A Sequence 1, Appli

Sequence:

Run on:

Searched:

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PCT-US94-08449A-4
US-09-344-27-5
US-08-311-743-2
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOKEY NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: ZymoGenetics, Inc. 1201 Eastlake Avenue
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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Sequence 16, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 2700, A
Sequence 27327, A
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              GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-20326
US-09-252-991A-24394
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US-09-252-991A-25921
US-09-252-991A-18853
US-09-252-991A-20358
                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                328717 seqs, 42310858 residues
                                                                                                                                                                                                                         1 ALAGWLRPEDGGQAEGAEDELEVR 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                        US-09-853-253-4
126
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Match Length
                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                             Scoring table:
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Database

Result No.

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                                                                                                                                                                                                                                                                                               COMPUTER: IDISACTE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 126; DB 3;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0;
US-09-046-479-2

Sequence 2, Application US/09046479

Petent No. 6291653

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Deisher, Theresa A.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 1,

Sequence

Sequence

Sequence Sequence Sequence

Sequence

-08-704-711A-1

-08-448-489-1

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APPLICANT: Zhang, Zemin Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: A Acids Encoding the Same FIER REFERENCE: P2730PIC13
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                           Length 117;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                        100.0%; Score 126; DB 4;
100.0%; Pred. No. 9.9e-12;
tive 0; Mismatches 0;
                     PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: 60/049787
PRIOR PAPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/062260
PRIOR FILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065710
PRIOR PILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/09996243 Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
                 1999-06-30
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Fong, Sherman
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                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier, Mary A.
Pan, James
  PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaton, Dan L.
                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                      ) NAME/KEY: SIGNAL
) LOCATION: (1)...(23)
US-09-608-810A-4
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                                                                                                      LENGTH: 117
                                                                                  SEQ ID NO 4
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APPLICANT:
                                                                                                                             TYPE: PRT
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APPLICANT:
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100.0%; Score 126; DB 4;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sociation of Application US/09608810A
Patent No. 642021
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Daslant, Theresa A.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
                       1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ALAGWLRPEDGGQAEGAEDEURYR 75
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                                                                                                                                             Sequence 2, Application US/08822897C Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/CDCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                       US-08-822-897C-2
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1998-05-07 NUMBER: 60/087106 1998-05-28 NUMBER: 60/087607 1998-06-02 NUMBER: 60/087609 1998-06-02 NUMBER: 60/08759 1998-06-02 NUMBER: 60/087827 1998-06-03 1998-06-04 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088021		1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1
ILING DATE: PPLICATION ILING DATE:	CATION CONTROL	ILLING DATE: ILLIN
PRIOR	PRIOR	PRIOR

PRIOR APPLICATION NUMBER: 60/08961
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-23
PRIOR PLILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09044
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-07-01
PRIOR PLILING DATE: 1998-07-02
PRIOR PLILING DATE: 1998-07-03
PRIOR PLILING DATE: 1998-07-03
PRIOR PLILING DATE: 1998-07-03
PRIOR PLILING DATE: 1998-

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APPLICANT: Tanzl, Rudolph E.
APPLICANT: Towacs, Dora M.
APPLICANT: Kovacs, Dora M.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-339-152A-16
Sequence 16, Application US/08339152A
Sequence 16, Application US/08339152A
Sequence 16, Application US/08339152A
Sequence 16, Application US/08339152A
Sequence 16, Application:
APPLICANT: Tanz1, Rudolph E.
APPLICANT: Tanz1, Rudolph E.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/339,152A FILING DATE: 10-NOV-1994 CLASSIFICATION: 435
         ; Sequence 17, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFRENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.78;
76.98;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-08-339-152A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20002
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                                                                                                                     US-08-339-152A-17
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| Sequence 23604, Application US/09252991A
| Patent No. 6551995
| GENERAL INFORMATION:
| APPLICANT MATC J. Rubenfield et al.
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
| CURRENT PELLING DATE: 1099-02-18
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR PILING DATE: 1998-02-18
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR FILING DATE: 1998-02-18
| NUMBER OF SEQ ID NOS: 33142
| LENTH: 518
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEUR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27758
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                                                                                                                                          Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 4; Length 518;
Pred. No. 13;
2; Mismatches 10; Indels
                                                                                                                                                                                       Indels
                                                                                                                                     100.0%; Score 126; DB 4; 100.0%; Pred. No. 9.9e-12;
                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 27758, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                                                                      1 ALAGWLRPEDGGQAEGAEDELEVR 24
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.3%; 72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                   Query Match
Best Local Similarity 100.07
Matches 24; Conservative
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203 GWLRPQDGSRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GWLRPEDGGQA 14
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-27758
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Matches
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Gaps

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APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Bupp, Keith
APPLICANT: Tanzi, Madolph
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: TAREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%; Score 50; DB 2; Length 653; 76.9%; Pred. No. 17; tive 1; Mismatches 2; Indels
                                                                                                                                                                        Score 50; DB 2; Length 653;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM:
CONFIGNTION FOR PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,276A
FILING DATE: 21-JAN-1996
FILING DATE: 21-JAN-1993
PRIOR APPLICATION NUMBER: US 07/830,022
FILING DATE: 20-APR-1992
PRIOR APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 20,021
REFERENCE/POCKET NUMBER: 20,021
REFERENCE/POCKET NUMBER: 20,021
REFERENCE/POCKET NUMBER: 0609.3520003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          US-08-689-276A-3
; Sequence 3, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
                                                                                                                                                                           39.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)371-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 653 amino acids
amino acid
                                             : 653 amino acids
amino acid
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 11 GGQAEGAEDELEV 23
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                 Best_Local Similarity 76.9
Matches 10; Conservative
  INFORMATION FOR SEQ ID NO:
                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
STREET: 1100 New YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                               US-08-007-999B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tall, Rudolph
APPLICANT: Tallonon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
TITLE OF INVENTION: THEREOF
WUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 1; Length 653; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTONINY/AGENT INFORMATION:
NAME: Steff, Eric X 6,688
REGISTRATION NUMBER: 36,688
REGISTRENCE/DOCKET NUMBER: 0609.4120000
TELECOMMUNICATION INFORMATION:
TELEPENA: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 20-JAN 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
TELLECOMMUNICATION INDERS: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08007999B Patent No. 5851787 GENERAL INFORMATION:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                               16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.78;
76.98;
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                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 653 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11:111 | 11 | 11
233 GGRAEGGEDEEEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 GGQAEGAEDELEV 23
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-152A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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Gaps

us-09-853-253-4.rai

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GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. RUBENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PELIOR DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
RIOR FILING DATE: 1999-07-27
NUMBER: OS 520 ID NOS: 33142
SEQ ID NO 29700
LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NESCULA (19-252-991A-20326)

Sequence 20226, Application US/09252991A

Sequence 20226, Application US/09252991A

Sequence 20226, Application US/09252991A

Sequence 20226, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PELICATION NUMBER: US/00/218

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20326

LENGTH: 405
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                                                                                                                                                              Score 48; DB 4; Length 428;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 405
                                                                                                                                                                                                          10; Indels
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Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-29700
; Sequence 29700, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                    293 LALWSLPEDPRPADWAADELSDR 315
                                                                                                                                                                                                                                                       2 LAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29700
                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGWLRPEDGGQAEGAED 19
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45.5%;
                                                                                                                                                           Query Match 38.1%;
Best Local Similarity 52.2%;
Matches 12; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 37.3%;
Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local Similarity 45.55
Matches 10; Conservative
  NUMBER OF SEQ ID NOS:
SEQ ID NO 19723
LENGTH: 428
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US-09-252-991A-20326
                                                                      TYPE: PRT
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Sequence 19723, Application US/09252991A

Sequence 19723, Application US/09252991A

Sequence 19723, Application US/09252991A

Sequence 10.651795

GENERAL INFORMATION:

APPLICAMTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: APERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
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Pred. No. 4.4;
1; Mismatches 4; Indels
                                                                                                                               US-08-039-198B-10
Sequence 10, Application US/08039198B
Patent No. 5888725
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEMIS, ALAN PETER
TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC. COMPALIA
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,198B
FLING DATE: 29-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/GB91/01744
FILING DATE: 08-OCT-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON CITY: ARLINGTON COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: WILSON, MARY J.
RECISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 139 amino acids
amino acid
                         11 GGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GWLRPEDGGQAEG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-039-198B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                   RESULT 11
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RESULT 15

US-09-252-914.24394

Sequence 24334, Application US/09252991A

Sequence 24394, Application US/09252991A

Sequence 24394, Application US/09252991A

Setent No. 6531795

GENERAL INFORMATION:

APPLICANT NO. 651705

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

WHOREN OF SEQ ID NOS: 33142

SEQ ID NO 24334

LENGTH: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.3%; Score 47; DB 4; Length 468; Best Local Similarity 57.9%; Pred. No. 34; Matches 11; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 11, 2003, 17:27:17 Job time : 7.41711 secs
                        5 WLRPEDGG--QAEGAEDELEVR 24
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CORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24394
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th 100.0%; Score 126; DB 9; Similarity 100.0%; Pred. No. 2.3e-10; 24; Conservative 0; Mismatches 0;
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US-09-997-653-268
US-09-997-667-268
US-09-990-438-268
US-09-990-562-268
US-09-990-571-268
US-09-990-111-268
US-09-990-111-268
US-09-990-156-268
US-09-991-157-268
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                                                                           US-09-991-181-268
US-09-989-730-268
US-09-990-436-268
US-09-993-687-268
US-09-989-734-268
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US-09-990-726-268
US-09-997-559-268
US-09-997-601-268
US-09-990-443-268
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US-09-997-628-268
US-09-997-683-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-853-253-4
; Sequence 4, Application US/09853253
; Peatent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: ZS1933-11ke Peptides
; FILE REFERENCE: 00-30
CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 2000-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALAGWLRPEDGGQAEGAEDELEVR 24
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US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
  ORGANISM: Homo sapiens
0.00.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.000.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Matches 2
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Sequence 2, Appli
Sequence 2, Appli
Sequence 268, App
                                                                                                                               September 11, 2003, 17:26:32 ; Search time 14.631 Seconds
(without alignments)
239.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: 'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: 'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: 'cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: 'cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: 'cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: 'cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                     Compugen Ltd
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US-09-794-987-2
US-09-853-253-2
US-09-989-723-268
US-09-989-729-268
US-09-989-73-268
US-09-989-73-268
US-09-991-73-268
US-09-991-73-268
US-09-991-73-268
US-09-991-73-268
US-09-991-73-268
US-09-991-163-268
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US-09-990-456-268
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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                                                                                                                                                                                                                                                                                                                                                            541936 segs, 145912426 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        1 ALAGWLRPEDGGQAEGAEDELEVR
                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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126
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Length 24; Indels ö

Gaps

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Length 117;
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      100.0%; Score 126; DB 9;
100.0%; Pred. No. 1.1e-09;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/067827
FILING DATE: 1998-66-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kljavin,Ivar J.
Napier,Mary A.
                                     Best Local Similarity 100. Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein, David
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Eaton, Dan L.
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US-09-989-722-268
            Query Match
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                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRALSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <un control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/09853253
| Patent No. US20020055156A1
| GENERAL INFORMATION:
| APPLICANT: JASPERS, STEPHEN
| APPLICANT: BEISHEN, THERESA
| APPLICANT: BISHOP, PAUL
| APPLICANT: BISHOP, PAUL
| TITLE OF INVENTION: 2sig33-like Peptides
| FILE REFERENCE: 00-00
| CURRENT PEPLICATION NUMBER: US/09/853,253
| CURRENT PELING DATE: 2001-05-10
| PRIOR FILING DATE: 2000-05-11
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEG ID NO 2
| LENGTH: 117
| TYPE: RRI
| GRANISM: HOMO Sapiens
                                                                                       CORRESPONDENCE ADDRESS:
RADBRESSER: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAWISIAK, DEBORDA:
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA: APPLICATION NUMBER: 09/046,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
98-09-794-987-2
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                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
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US-09-853-253-2
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NUMBER: 60/088025	NUMBER: 60	1998-06-04	998-06-04	NUMBER: 60/088029 1998-06-04	MBER: 6	98-06- BER: 6	8-06-04	MBER: 00/08632 998-06-04	NUMBER: 60/088167	BER: 6	1998-06-05	998-06-05	NUMBER: 60/088217	BER: 60	1998-06-09	NUMBER: 60/088/34 1998-06-10	NUMBER: 60	1998-06-10	1998-06-10	NUMBER: 60	TABB-DP-T	1998-06-10	NUMBER: 60/088826	996-00-1 MBER: 60	1998-	мьек: 50/08866 998-06-11	NUMBER: 60/088876	MBER: 60	998-06-12	NUMBER: 60/089440 1998-06-16	MBER: 60	998-06- MBFB· 6	998-06-16	NUMBER: 60/089532	MBER: 60	1998-06-17 Nimber 607089598	998-06-17	NUMBER: 60/089599	BER:	998-06-17	NUMBER: 60/089653 1998-06-17	NUMBER: 6	1998-06-18	998-06-18	MBER: 60	98-00- BER: 6	998-06-19	9	MBER: 60
APPLICATION FILING DATE:	PPLICATION	FILING DATE:	ILING DA		PPLICATI	APPLICATION	FILING DATE:	ILING DA	APPLICATION FILING DATE:	PPLICA	FILING DATE:	ILING DA	APPLICATION FILING DATE:	PPLICATIO	ILING DA	FILING DATE:	PPLICATION	FILING DATE:	ILING DAT	PPLICATION	APPLICATION	ILING DAT	ATI	PPLICATIO	FILING DATE:	ILING DA	PPLICATIO	ζĤ	ILING DAT	PPLICAT ILING D	PPLICATIO	FILING DATE:	ILING DAT	PPLICAT	PPLICATIO	APPLING DATE:	ILING DA	APPLICATION FILING DAFF.	PPLICATI	ILING DA	FILING DATE:	PPLICATION	FILING DATE:	ILING DA	PPLICATI	APPLICATION	ILING DA	PPLICATI	CA
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PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: 60/090252
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
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PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PRILING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07

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Gaps

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Length 117; Indels

Ouery Match 100.0%; Score 126; DB 9; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 24; Conservative 0; Mismatches 0;

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R APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088126

R APPLICATION NUMBER: 60/088167

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088127

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/08855

R APPLICATION NUMBER: 60/088655

R APPLICATION NUMBER: 60/088655
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R APPLICATION NUMBER: 60/088742

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R APPLICATION NUMBER: 60/08810

R RILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08824

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R FILING DATE: 1998-06-17
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
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R APPLICATION NUMBER: 60/089908
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089947
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
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APPLICATION UNBER: 60/089105
APPLICATION NUMBER: 60/089440
APPLICATION NUMBER: 60/089440
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APPLICATION UNMBER: 60/088861
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-04
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CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-24

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-04-28

PRIOR PILING DATE: 1998-04-28

PRIOR PILING DATE: 1998-04-28
                                                                                                    Sequence 268, Application US/09989723 Patent No. US20020072092A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/087759
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APPLICATION UNMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William II
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Godowski, Paul J.
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Napier, Mary A.
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US-09-989-723-268
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998-06-19

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Godowski, Paul J.
Grimaldi, J.Christopher
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Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                     Ferrara, Napoleone
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                                                                Botstein, David
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                                                                                                Desnoyers, Luc
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                                                                                                                                                                                        PRIOR FILING DATE: 1998-06-24
PRIOR PELLAGATION NUMBER: 60/090435
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090445
PRIOR PELLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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PRIOR PELLANG DATE: 1998-06-24
PRIOR PELLANG DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090535
PRIOR PELLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR PELLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PELLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PELLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PELLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/091696
PRIOR APPLICATION NUMBER: 60/091696
PRIOR APPLICATION NUMBER: 60/091696
PRIOR PELLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091696
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09193
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PILING DATE: 1998-06-24
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Best Local Similarity 100.0%;
Matches 24; Conservative (
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides Currern Application Number: 2001-11-19
PRIOR PILLIAGION NUMBER: 05/046586
PRIOR PILLIAGION NUMBER: 05/065260
PRIOR PILLIAGION NUMBER: 05/065310
PRIOR PILLIAGION NUMBER: 05/065311
PRIOR PILLIAGION NUMBER: 05/069106
PRIOR PILLIAGION NUMBER: 05/099106
PRIOR PILLIAGION NUMBER: 05/099109
PRIOR

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Indels

0; Mismatches

52 ALAGWLRPEDGGQAEGAEDELEVR 75

US-09-989-279-268 . Sequence 268, Application US/09989279 . Patent No. US20020072496A1 ; GENERAL INFORMATION:

1 ALAGWLRPEDGGQAEGAEDELEVR 24

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R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R APPLICATION NUMBER: 60/089947
R APPLICATION NUMBER: 60/089947
R FILING DATE: 1998-06-19
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R FILING DATE: 1998-06-22
R PILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R PILING DATE: 1998-06-22
R PILING DATE: 1998-06-22
R PILING DATE: 1998-06-22
R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088202

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088212

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/08655

R APPLICATION NUMBER: 60/08655

R APPLICATION NUMBER: 60/08655
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R FILING DATE: 1998-06-10
A PPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088858
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
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R PELING DATE: 1998-06-17
R PELING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
FYLING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090431
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| PRIOR APPLICATION NUMBER: 66,09044
| PRIOR APPLICATION NUMBER: 66,09044
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| PRIOR PLINKO DATE: 1998-06-23
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| PRIOR PRIOR DATE: 1998-07-01
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A PELLING DATE: 1998-06-09
A APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R PILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/088824

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08826

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088858

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11

R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/089560

R PILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089801

R APPLICATION NUMBER: 60/089801

R APPLICATION NUMBER: 60/089908

R PILING DATE: 1998-06-18

R PILING DATE: 1998-06-18

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R PILING DATE: 1998-06-19

R PPLICATION NUMBER: 60/089948

R PILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
LICATION NUMBER: 60/088655
ING DATE: 1998-06-09
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-24
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Chang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: 00/09/387
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-07
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/081302
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-06-28
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PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/08021
PRIOR APPLICATION NUMBER: 60/08025
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08026
PRIOR APPLICATION NUMBER: 60/08026
PRIOR APPLICATION NUMBER: 60/08026
PRIOR APPLICATION NUMBER: 60/08026
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
PRIOR FILING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/08033
PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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APPLICATION UNMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
                                         Godowski, Paul<sup>'</sup>J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A
Tumas, Daniel
erritsen, Mary E.
                                                                                                                                                                                   Paoni, Nicholas F.
                                                                                                               (ljavin, Ivar J
                                                                                                                                   Napler, Mary A.
                                                                                                                                                                Pan, James
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APPLICANT: Wood, Walliam, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: 05/04/987
PRIOR FILING DATE: 1997-10-11
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1998-01-26
PRIOR FILING DATE: 1998-01-26
PRIOR PRIOR APPLICATION NUMBER: 60/08025
PRIOR FILING DATE: 1998-01-26
PRIOR PRIOR APPLICATION NUMBER: 60/08025
PRIOR PRIOR APPLICATION NUMBER: 60/08033
PRIOR FILING DATE: 1998-01-26
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
                                                                                                                              Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin
                                                                 Roy, Margaret Ann
Stewart, Timothy A.
                                             Paoni, Nicholas F.
    Napier, Mary A.
                                                                                                          Tumas, Daniel
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APPLICANT:
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                                 R APPLICATION NUMBER: 60,090535
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60,090540
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60,090542
R FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                       R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
R PELLING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/09182
R FILING DATE: 1998-07-07
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: Sequence 268, Application US/09989731
: Patent No. US20020103125A1
: GENERAL INFORMATION:
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
                                                                                                                                                                                                                  APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/090472
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 100.
Matches 24; Conservative
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Eaton, Dan L.
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APPLICANT: APPLICANT:

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A PAPLICATION NUMBER: 60/08926

R APPLICATION NUMBER: 60/08861

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R APPLICATION NUMBER: 60/089105

R APPLICATION NUMBER: 60/089512

R APPLICATION NUMBER: 60/089512

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R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089518

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089518

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/090246

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-13

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-22

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090445

R APPLICATION NUMBER: 60/090444

R APPLICATION NUMBER: 6
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/090542
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100.0%; Pred. No. 1.1e-09;
iive 0; Mismatches 0;
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R APLICATION NUMBER: 60/090557

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090676

R APLICATION NUMBER: 60/090678

R APLICATION NUMBER: 60/090690

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25

R APLICATION NUMBER: 60/090696

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

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R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-26

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R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091519

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091626

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091626

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091636

R FILING DATE: 1998-07-02

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091636

R FILING DATE: 1998-07-02

R FILING DATE: 1998-07-02
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R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R RELING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R R FILING DATE: 1998-07-07
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Best Local Similarity 100.
Matches 24; Conservative
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Sequence 268, Application US/09989732 patent No. US20020123463A1; GENERAL INFORMATION: Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Ferrara, Napoleone APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. Botstein, David Desnoyers, Luc Eaton, Dan L APPLICANT:
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Grimaldi, J. Christopher Gurney, Austin L. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K Paoni, Nicholas F. Kljavin, Ivar J. Napier, Mary A. APPLICANT APPLICANT APPLICANT

Godowski, Paul

APPLICANT: APPLICANT:

APPLICANT

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R APPLICATION NUMBER: 60/088976
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R RPLING DATE: 1998-06-16
R FILING DATE: 1998-06-16
R R APPLICATION NUMBER: 60/089512
R APPLICATION NUMBER: 60/089514
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R APPLICATION NUMBER: 60/089514
                    APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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                                  APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT PAPLICATION NUMBER: US/09/989,732

CURRENT FILING DATE: 2001-11-19

PRIOR PAPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-14

PRIOR FILING DATE: 1997-11-14

PRIOR PAPLICATION NUMBER: 60/06570

PRIOR PAPLICATION NUMBER: 60/056710

PRIOR PAPLICATION NUMBER: 60/056710
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R FILING DATE: 1998-06-04
R PAPLICATION NUMBER: 60/088326
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088167
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R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R PAPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
R FILING DATE: 1998-06-02
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R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087827
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R FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-03-20
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
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FILING DATE: 1998-60-04
PPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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NG DATE: 1998-06-09
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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Williams, P. Mickey Wood, William I.
APPLICANT:
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R APPLICATION NUMBER: 60/062250
R FILING DATE: 1997-10-17
R FILING DATE: 1997-11-12
R FILING DATE: 1997-11-12
R FILING DATE: 1997-11-12
R FILING DATE: 1997-11-13
R FILING DATE: 1997-11-13
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/065910
R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
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R FILING DATE: 1998-06-07
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R APPLICATION NUMBER: 60/087607
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/08759
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/08021
R APPLICATION NUMBER: 60/08021
R APPLICATION NUMBER: 60/08021
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08025
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08026
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R APPLICATION NUMBER: 60/08028
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R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088126

R APPLICATION NUMBER: 60/088167

R APPLICATION NUMBER: 60/088167

R APPLICATION NUMBER: 60/088128

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

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R FILING DATE: 1998-06-05

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R APPLICATION NUMBER: 60/088217
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R APPLICATION NUMBER: 60/089738
R APLICATION NUMBER: 60/089742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08810
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APPLICATION NUMBER: 60/088030
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Pred. No. 1.1e-09;
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                                       PRIOR APLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09062
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090690
                      FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
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Grimaldi,J.Christopher
Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 24; Conservative
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APPLICANT: Ashkenazi, Avi J.
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fong, Sherman
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PRICE RILING DATE: 1998 06 12
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PRICE PRICE PATION NUMBER: 60/089512
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PRICE RILLING DATE: 1998 06 17
PRICE RILLING DATE: 1998 06 19
PRICE RILLING DATE: 1998 06 23
PRICE RILLING DATE:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730p1012 acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/990,442 CURRENT FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/049787 PRIOR PLICATION NUMBER: 60/062250 PRIOR PLING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/062250 PRIOR APPLICATION NUMBER: 60/062186 PRIOR PLING DATE: 1997-11-12 Gaps ö Length 117; Indels Query Match 100.0%; Score 126; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 24; Conservative 0; Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PRILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09154
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PRILICATION NUMBER: 60/091626
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PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 1 ALAGWLRPEDGGQAEGAEDELEVR 24 52 ALAGWLRPEDGGQAEGAEDELEVR 75 Sequence 268, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J.Christopher Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I. Zhang, Zemin Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Gurney, Austin L. Kljavin, Ivar J. Napier, Mary A. Pan, James Paon1, Nicholas F. US-09-990-442-268 APPLICANT: WAPPLICANT: WAPPLICANT: WAPPLICANT: WAPPLICANT: WAPPLICANT: Z APPLICANT:
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PRIOR APPLICATION NUMBER: 60,7065311
PRIOR APPLICATION NUMBER: 60,706570
PRIOR APPLICATION NUMBER: 60,707545
PRIOR PLINK DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
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PRIOR FILING DATE: 1998-05-29
PRIOR PRIOR FOLING DATE: 1998-05-20
PRIOR PRIOR CAPILOR DATE: 1998-05-20
PRIOR PLINK DATE: 1998-05-20
PRIOR PRIOR DATE: 1998-05-20
PRIOR PLINK DATE: 1998-05-20
PRIOR PLINK DATE: 1998-05-20
PRIOR PLINK DATE: 1998-06-20
PRIOR PLINK DATE: 1998-06-10
PRIOR PLINK DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-17

PRIOR PLILING DATE: 1998-06-18

PRIOR PLILING DATE: 1998-06-19

PRIOR PLILING DATE: 1998-06-12

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PRIOR PLILING DATE: 1998-06-12

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PRIOR PLILING DATE: 1998-06-24

PRIOR PLILING DATE: 1998-06-25

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R FILING DATE: 1998-05-28

R APPLICATION NUMBER: 60/08/507

R FILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/08/759

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R FILING DATE: 1998-06-03
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R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/086028

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-04

A RPPLICATION NUMBER: 60/086030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086033
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RILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
RILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
RILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
RILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-11
R PILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
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                    APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-17
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Pred. No. 1.1e-09;
; Mismatches 0;
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                                    PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/091082
PRIOR FILING DATE: 1998-07-07
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A APPLICATION NUMBER: 60/062250

PR FILING DATE: 1997-10-17

PR APPLICATION NUMBER: 60/065186

PR FILING DATE: 1997-11-12

PR APPLICATION NUMBER: 60/065311

PR FILING DATE: 1997-11-13
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Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
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FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
APPLICATION NUMBER: 60/091478
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Grimald1, J. Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watnabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Fong, Sherman
Gerber, Hanspeter
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Goddard, Audrey
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Kljavin, Ivar J.
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Botstein, David
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Pan, James
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Eaton, Dan L.
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PRIOR RAPLICATION WUMBER: 60/08599

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PRIOR PAPLICATION WUMBER: 60/08560

PRIOR PALLICATION WUMBER: 60/08561

PRIOR PALLICATION WUMBER: 60/08561

PRIOR PALLICATION WUMBER: 60/08561

PRIOR PALLICATION WUMBER: 60/08968

PRIOR PALLICATION WUMBER: 60/08962

PRIOR PALLICATION WUMBER: 60/09043

PRIOR PALLICATION WUMBER: 60/09044

PRIOR PALLICATION WUMBER: 60/09064

PRIOR PALLICATION WUMBER: 60/09069

PRIOR PALLICATION WUMBER: 60/0
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CURRENT APPLICATION NUMBER: US/09/993,604
PRIOR PELICATION NUMBER: 60/049787
PRIOR PELICATION NUMBER: 60/045186
PRIOR FILING DATE: 1997-06-16
PRIOR PELICATION NUMBER: 60/065111
PRIOR PELICATION NUMBER: 60/065111
PRIOR PELICATION NUMBER: 60/065311
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PRIOR PELICATION NUMBER: 60/065311
PRIOR PELICATION NUMBER: 60/06570
PRIOR PELICATION NUMBER: 60/065310
PRIOR PELICATION NUMBER: 60/075945
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenal, Avi J.
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Pan, James
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US-09-993-604-268
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PRIOR FILING DATE: 1998-06-18
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PRIOR PRILICATION NUMBER: 60/089907
PRIOR PELLING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089917
PRIOR APPLICATION NUMBER: 60/089918
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089918
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-23
PRIOR PRILING DATE: 1998-06-23
PRIOR PRILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-07-01
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R APPLICATION NUMBER: 60/088025
R APPLICATION NUMBER: 60/088025
R APPLICATION NUMBER: 60/088025
R APPLICATION NUMBER: 60/088026
R APPLICATION NUMBER: 60/088028
R APPLICATION NUMBER: 60/088029
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030
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R APPLICATION NUMBER: 60/088031
R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/08655

R APPLICATION NUMBER: 60/08655

R APPLICATION NUMBER: 60/086734

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08738

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088742

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088810

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088824

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088861

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088976

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088976

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/089976

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089976

R APPLICATION NUMBER: 60/089512

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R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R PILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089509

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089609

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089619

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089619

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R FILING DATE: 1998-06-04
A PPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088202
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R FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-26
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-08
PRIOR PILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-05-07
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Pred. No. 1.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 268, Application US/09990456 Patent No. US20020137890A1 GENERAL INFORMATION: APPLICANT: Ashkenazi,Avi J. APPLICANT: Baker,Kevin P. APPLICANT: Baker,Kevin P. APPLICANT: Baker,Levin D. APPLICANT: Desnoyers,Luc
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/087827
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
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Best Local Similarity 100.0%;
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Williams, P. Mickey
Wood, William I.
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Tumas, Daniel
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Gerritsen, Mary E
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Pan, James
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Eaton, Dan L.
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-06
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/08460
PRIOR FILING DATE: 1998-01-06
PRIOR APPLICATION NUMBER: 60/08460
PRIOR APPLICATION NUMBER: 60/08460
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PRIOR PILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08760
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08760
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08760
PRIOR PRILICATION NUMBER: 60/08760
                                                                                                                             Sequence 268, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
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APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Fong, Sherman
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Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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Botstein, David
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Eaton, Dan L.
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US-09-989-721-268
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DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090695

DR APPLICATION NUMBER: 60/090862

DR APPLICATION NUMBER: 60/090862

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-06-26

DR FILING DATE: 1998-06-10

DR FILING DATE: 1998-06-10

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR APPLICATION NUMBER: 60/091544
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R FILING DATE: 1998-07-02
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R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-23
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PR FILING DATE: 1998-06-24

PR APPLICATION NUMBER: 60/090444

PR FILING DATE: 1998-06-24

PR FILING DATE: 1998-06-24
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RR APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
RR APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/088858
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R FILING DATE: 1998-66-11
R APPLICATION NUMBER: 60/08876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089876
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089470
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R APPLICATION NUMBER: 60/089599

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R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089653

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089601

R FILING DATE: 1998-06-18

R FILING DATE: 1998-06-18

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R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/08952
APPLICATION NUMBER: 60/090246
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-22
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R FILING DATE: 1998-06-23
R PAPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-23
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R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-24 RELIGIO DATE: 1998-06-25

REPLICATION NUMBER: 60/090678

RELIGING DATE: 1998-06-25

REPLICATION NUMBER: 60/090690

REFLICATION NUMBER: 60/090694

RELIGING DATE: 1998-06-25

REPLICATION NUMBER: 60/090695

RELIGING DATE: 1998-06-25

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REPLICATION NUMBER: 60/091478

REPLICATION NUMBER: 60/091549

REPLICATION NUMBER: 60/091549

REPLICATION NUMBER: 60/091549

REPLICATION NUMBER: 60/091626

REPLICATION NUMBER: 60/091633

REPLICATION NUMBER: 60/091978

REPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 PRESENTATION OF PRINCIPLE PRIOR PRIOR PRIOR

1 ALAGWLRPEDGGQAEGAEDELEVR 24

Query Match 100.0%; Score 126; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 24; Conservative 0; Mismatches 0;

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Gaps

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Length 117; Indels

52 ALAGWLRPEDGGQAEGAEDELEVR 75

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Search completed: September 11, 2003, 17:48:31 Job time : 14.631 secs

Sequence 158, App Sequence 25687, A Sequence 4, Appl1 Sequence 4, Appl1 Sequence 12896, A Sequence 19, Appl Sequence 2, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 2, Appl Sequence 2, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 21, A

US-09-325-91A-158 US-09-252-91A-25687 US-09-444-664-4 US-09-414-664-4 US-09-252-91A-22896 US-09-252-91A-17695 US-09-207-388-19 US-09-464-483-2 US-09-444-664-2 US-08-444-664-2 US-08-444-664-2 US-08-531-601-1 US-08-859-032-1 US-08-859-032-1 US-09-207-388-22 US-09-207-388-22 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24 US-09-207-388-24

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2; Search time 7.87166 Seconds (without alignments) 123.627 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Post-processing: Listing first 45 summaries

Issued_Patents_AA:*

Database

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ALIGNMENTS	A. A. HOMOLOGS HOMOLOGS dows Version 2.0 /046,479 97-04 N:	Ouery Match 100.0%; Score 23; DB 3; Length 117; Best Local Similarity 100.0%; Pred. No. 2.8e-15; Matches 23; Conservative 0; Mismatches 0; Indels

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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT PAPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR PILING DATE: 1997-06-16
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PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
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PRIOR PILING DATE: 1998-02-25
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Grimaldi, J.Christopher
Gurney, Austin L.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kljavin,Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eaton, Dan L.
                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                             ; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-996-243-268
                                                                                                             LENGTH: 117
                                                                                                                                      TYPE: PRT
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APPLICANT:
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APPLICANT:
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APPLICANT:
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1 Similarity 100.0%; Pred. No. 2.8e-15;
23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: PRESESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,897C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Delsher, Theresa A.
APPLICANT: Blshop, Paul D.
TITLE OF INVENTION: SGIP PEPTIDES
FILE REFERENCE: 99-51
CURRENT APPLICATION NUMBER: US/09/608,810A
CURRENT FILING DATE: 2000-06-30
                                                                                                                                          Sequence 2, Application US/08822897C

Patent No. 6380158

GENERAL INFORMATION:
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
1 ALAGWLRPEDGGQAEGAEDELEV 23
                         52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ALAGWLRPEDGGQAEGAEDELEV 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/CDCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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Best Local Similarity
Matches 23; Conserva
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COUNTRY: USA
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                       Seattle
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                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                               US-08-822-897C-2
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PRIOR FILING DATE: 1398-06-07
PRIOR FILING DATE: 1398-06-02
PRIOR PRIOR PAPEL (1998-06-02
PRIOR PRIOR PAPEL (1998-06-03
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PRIOR PRIOR PAPEL (1998-06-03
PRIOR PRIOR PAPEL (1998-06-03
PRIOR PRIOR PRIOR PRIOR (1998-06-04
PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/089601
PRIOR APPLICATION NUMBER: 60/08901
PRIOR FILING DATE: 1998-66-18
PRIOR FILING DATE: 1998-66-18
PRIOR PAPLICATION NUMBER: 60/08940
PRIOR PELLON FOUNDER: 60/08940
PRIOR FILING DATE: 1998-66-18
PRIOR FILING DATE: 1998-66-18
PRIOR FILING DATE: 1998-66-19
PRIOR PELLONION NUMBER: 60/08948
PRIOR FILING DATE: 1998-66-19
PRIOR PELLONION NUMBER: 60/08948
PRIOR PILING DATE: 1998-66-12
PRIOR PELLONION NUMBER: 60/08948
PRIOR PILING DATE: 1998-66-12
PRIOR PELLONION NUMBER: 60/09024
PRIOR PELLONION NUMBER: 60/09034
PRIOR PILING DATE: 1998-66-22
PRIOR PILING DATE: 1998-66-24
PRIOR PILING DATE: 1998-66-25
PRIOR PILING DATE: 1998-66-26
PRIO

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GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. RUBENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: MUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20368
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16798, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. RUbenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
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Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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5.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.4%; Score 7; DB 4;
100.0%; Pred. No. 25;
tive 0; Mismatches
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100.0%; Pred. No.
                                                                                                          US-09-252-991A-20368
; Sequence 20368, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16798
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SEQ ID NO 16798
LENGTH: 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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                             22 DGGQAEG 28
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US-08-428-488-13
                                                                                              RESULT 7
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-07
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27032
LENGTH: 552
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                                                                                                                                   Length 117;
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                                                                                                                                                                                  0; Indels
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                                                                                                                                   Score 23; DB 4; I
Pred. No. 2.8e-15;
; Mismatches 0;
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Pred. No. 20;
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100.0%; Pred. No. 24;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 3033, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Staphylococcus epidermidis
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-09
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100.0%; Pre
0;
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100.0%; Pre
ltive 0; 1
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27032
                                                                                                                                                                              23; Conservative
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                   Query Match
Best Local Similarity
Matches 23; Conserva
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US-09-134-001C-3033
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DGGQAEG 16

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APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
APPLICANT: Blanche, Jotal
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Parricia
APPLICANT: Lacroix, Parricia
APPLICANT: Lacroix, Parricia
APPLICANT: Lacroix, Parricia
APPLICANT: Debussche, Laurent
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: Comversion: Coding For These Polypeptides And Their Use
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                 E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
APPLICATION DATA:
APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGIGSTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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100.0%; Pred. No. 49;
iive 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 6; Conservative
                                                                  STREET: 1300 I St
CITY: Washington
STATE: D.C.
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STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
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2 QAEGAE 7
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US-08-510-646B-32
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NENTION: Polypeptides Involved In The
VENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
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TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: /note- "Position 30 = Glu-NH2." US-08-428-488-13
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                      ADDRESSEE: Burns, Doane, Swecker 6 Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia STATE: Virginia STATE: Virginia STATE: Virginia STATE: Virginia STATE: Virginia STATE: STATE: Polymera STATE: COMPUTER FROMBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS OFFWARE: Patentin Release #1.0, Version #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 314
ATTORNEY/AGENT INFORMATION:
NAME: BRUMELSTER, MARY KAtherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 anino acids
TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanck, Veronique
APPLICANT: Blanche, Francis
APPLICANT: CROUZEL, JOGH
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
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Zagorec, Monique
Debussche, Laurent
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LOCATION: 30
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Best Local Similarity 100.0
                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Door
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26 GAEDEL 31
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APPLICANT:
APPLICANT:
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APPLICANT:
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Patent No. 6514755
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A
CURRENT FILING DATE: 2000-10-06
PRIOR PILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 09/135,994
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Fatent No. 6280938
GENERAL INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER APPLICATION NUMBER: 60/056,170
SAPTWARE: PALING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12
LENGTH: 129
                                                                                                                                                                                                                         NAME: MAGNES, Kenneth J.
NAME: MAGNES, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 aming acids
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100.0%; Pred. No. 62;
ilve 0; Mismatches
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                        FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
   US/08/403,852
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100.0%;
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Best Local Similarity 100.
Matches 6; Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 6; Conserv
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1300 I Street, N.W., Suite 700
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
                           PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 49;
tive 0; Mismatches
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                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PREIGRATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 25-5EP-193
PRIOR APPLICATION DATA:
FILING DATE: 25-5EP-193
PRIOR APPLICATION DATA:
FILING DATE: 25-5EP-1992
ATTORNEY AGENT INFORMATION:
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806
TELECOMMULCATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 antho acids
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Lacroix, Patricia
Thibaut, Denis
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Blanche, Francis
Crouzet, Joel
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Best Local Similarity 100.
Matches 6; Conservative
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RESULT 15

US-09-198-452A-612

US-09-198-452A.

Sequence 612, Application US/09198452A.

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: GITIFIALS.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering the patent of the patent 
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26.1%; Score 6; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.1%; Score 6; DB 4; Length 129; Best Local Similarity 100.0%; Pred. No. 62; Matches 6; Conservative 0; Mismatches 0; Indels
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; PRIOR FILING DATE: 1998-08-18; NUMBER OF SEQ ID NOS: 14; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 12; LENGTH: 129; TYPE: PRT; ORGANISM: Homo saplens US-09-684-843A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-612
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Human secreted/tra
Novel secreted and
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Human preproghrell
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Membrane-bound pro
Human PRO 1066 poly
Human PRO1066 (UNO)

Human polypeptide
Bovine ghrelin pre
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
SnpR activator pro
Amino acid sequenc
Staphylococcus api
Drosophila melanog
Human peptide #168

PD-1_Ctail2 peptid Neutrophil-activat

Deisher TA, Bishop PD;

Jaspers SR, Sheppard PO,

WPI; 2002-443750/47

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Human, zsig33-like peptide, gastric contractility, nutrient uptake, growth hormone, digestive enzyme, restorative therapy; gene therapy, protein therapy; gastrointestinal, endocrine, anabolic.
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ABUG9066
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AAE23838
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AAB60523
AAG29677
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AAG29675
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  10-MAY-2001; 2001US-0853253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JASP/) JASPERS S R. (SHEP/) SHEPPARD P O. (DEIS/) DEISHER T A. (BISH/) BISHOP P D.
JS2002055156-A1.
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 RESULT 1
AAE23840
  Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human zsig33-linke
Human exon 3-delet
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Protein designated
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150.669 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                             OM protein - protein search, using sw model
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AAE15885
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The invention relates to z81933-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate Z31G33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The Z31G33 peptides are used as antigens in need of restorative therapy. The Z31G33 peptides are used of antibodies against 251G33 and in assays to identify modulators of Z31G33 expression and activity. The anti-Z31G33 antibodies are also used as diagnostic agents for detecting the presence of Z31G33 in samples (e.g. by enzyme inked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or acids of digestive enzymes and acidical secretion of enzymes and/or hormones in the pancreas. S21933-like DNA is used in gene therapy and s21933-like peptide. Is human zs1933-like peptide.
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             2SIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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100.0%; Pred. No. 5.9e-15;
.ive 0; Mismatches 0;
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                                                                                        Claim 1; Page 28; 34pp; English.
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DEISHER T A.
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Best Local Similarity
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(DEIS/)
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The hyportion relates to Zayljarinke peptitos and Little tourisepouling nucleic acids and methods for modulating qastric contractility, nutrient uptake, growth hormones, secretion of digastive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as the nucleic acids of the invention and their complements are used as consistent of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 and in assays to identify medulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG331 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or hormones in the pancreas zsig33-like DNA is used in gene therapy and zsig33-like peptide. The peptide, as zsig33-like peptide.
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                                                                                                     The invention relates to zsig33-like peptides and their corresponding
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contractility, nutrient uptake, growth hormones and/or secretion digestive/pancreatic enzymes and hormones ^{\rm -}
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100.0%; Pred. No. 5.9e-15;
iive 0; Mismatches 0;
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                                                              Claim 1; Page 28; 34pp; English.
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N-PSDB; AAD25760.
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Matches 23; Conserv
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AAE15885
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Bishop PD;

Deisher TA,

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stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. Zs331P peptides, nucleic acids and/or antibodies are useful for treating disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal motility, recruitment of digestive enzymes, inflammation and regulation of nutrient absorption. Sequences of the invention are useful in gene therapy. The present sequence is human zsig33-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to zsig33-like peptides (2S33LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and zsig33-epsilon peptides and nucleic acid molecules encoding such zsig33-like peptides. Zs32LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and isolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypodylycaemic preparations containing glucose and as adsorption the additive for oral days which require fast nutrient action and to
                                                                                                                                                                                                                                         New polypeptides, useful for modulating gastric contractility, nutrient uptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises
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                                                                                                                                                                                                                                                                                                                                                                                                Claim 1c; Page 82; 89pp; English
                                                                                           Jaspers SR, Sheppard PO,
                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                    zsig33-like peptides
                                                                                                                                                    WPI; 2002-082982/11
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                                                                                                                                       zsig33-linker, zsig33-beta, zsig33-linker peptides calculate and zsig33-linker, zsig33-beta, zsig33-linker, zsig33-beta, zsig33-geptides activate the immune system in boosting immunity to infectious alseases, treating immunocompromised patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines and in treatment of bacterial, viral, protozoal and improving vaccines and in treatment of bacterial, viral, protozoal and isolate receptors involved in growth regulation in the liver, blood vealuating functions of hypothalamus-pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to antienhanders for oral drugs which require fast nutrient action and to simulate glucose and as adsorption enhancers for oral drugs which require fast nutrient action and to stimulate glucose induced insullin release. They are also useful as the expansion, differentiation, growth factor and hormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These molecules are useful for treating dysfunction associated with contractile tissues or to suppress or enhance contractility in vivo and to treat gastrointestinal and growth related diseases. ZS33LP peptides, nucleic acids and or antibodies are useful for treating dysfunction associated acids and growth related diseases. ZS33LP peptides, nucleic
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                                                                                                                       invention relates to zsig33-like peptides (2S33LP) including
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                                                               Claim 1b; Page 81; 89pp; English.
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Length 23;
                                               Indels
100.0%; Score 23; DB 23;
100.0%; Pred. No. 5.9e-15;
tive 0; Mismatches 0;
                                                                                            1. ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                          Location/Qualifiers
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                         Best Local Similarity 100.
Matches 23; Conservative
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Homo sapiens
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In human zsig33-like peptide, zsig33-linker peptide.
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                                                                                                                                                                                                                                                 ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
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                                                                                                                                                                                       Deisher TA, Bishop PD;
 /note= "Hydrophilic region"
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                                                                                                                                                                                                                                                                                                    Claim 1; Page 28; 34pp; English.
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                                                                                                 11-MAY-2000; 2000US-203300P
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                                                                                                                                                                                       Jaspers SR, Sheppard PO,
                                                                                                                         ) JASPERS S R.
) SHEPPARD P O.
) DEISHER T A.
                                                                                                                                                                                                              WPI; 2002-443750/47.
N-PSDB; AAD38239.
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nes 23; Conserva
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The invention relates to zsig33-like peptides (zS31LP) including zsig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and scassig33-linker, zsig33-beta, zsig33-gamma, zsig-33-delta and such zsig33-like peptides and nuclaic acid moleculas encoding auch zsig33-like peptides. ZS31LP peptides activate the immune system in boosting immunity to infectious diseases, treating immunocompromised to patients such as human immunodeficiency virus (HIV) patients, in improving vaccines and in treatment of bacterial, viral, protozoal and fungal infections. Peptides of the invention are used to identify and consolate receptors involved in growth regulation in the liver, blood vessel formation and other developmental processes. They are useful for evaluating functions of hypothalamus pituitary-adrenal axis, to modulate growth and/or differentiation of tumour cells, as additives to anti-hypoglycaemic preparations containing glucose and as adsorption chhomocers for oral drugs which require fast nutrient action and to stimulate glucose-induced insulin release. They are also useful as research reagents for the expansion, differentiation, growth factor and chormone secretion and/or cell-cell interactions of tissues associated with gastrointestinal system, brain and central nervous system. These colorentials are useful for treating disorders associated diseases. ZS31LP peptides, nucleic and color and contractility in vivo and to treat catch and/or antibodies are useful for treation of diseases. ZS31LP peptides, nucleic with mastrointestinal and growth related diseases. ZS31LP peptides, or with mastrointestinal parameter of the contraction of diseases.
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ive 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 23; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide.
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Homo sapiens.

14-NOV-2002

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are concentration in cells. The peptides are ghrelin homologues and are concentrated in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth commone deficiency. The compounds of the invention are safe with an accompanying side effects. The present sequence represents a ghrelin-type growth hormone secretagogue (GHS) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                     New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
                                                                                                                                                                                                                                                              Hosoda H, Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 22;
100.0%; Pred. No. 2.3e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "signal peptide"
24..117
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 186-187; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ALAGWLRPEDGGQAEGAEDELEV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW87991 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                 of infant growth disorders -
                                                                                                                               23-JUL-1999; 99JP-0210002.
29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                    24-JUL-2000; 2000WO-JP04907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein designated zsig33.
                                                                                                                                                                                                                                                              Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                      WPI; 2001-159704/16
                                                                                                                                                                                                                    (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF59647
  WO200107475-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                              01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW87991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW8799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
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                                                                                                                                                                   Ghrelin, preproghrelin, GHS-R 1b, benign prostatic hyperplasia, therapy, breast, cervical, uterine, choriocarcinoma, prostate, ovary, cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exon-3 deleted preproghtelin and/or a GHS-H b protechis or nucleic acids. The antibodies, exon 3-deleted form of preproghtelin and antagonists are useful for treating cancer of the reproductive system such as prostate, owarian, breast, cervical or uterine cancer, choricoratinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein; calclum concentration elevation; infant growth disorder; growth hormone deficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 24;
Pred. No. 1.9e-14;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herington AC;
                                                                                                                          Human exon 3-deleted ghrelin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB60517 standard; Protein; 116 AA
AAE33410 standard; Protein; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 34; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1b proteins or nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2001; 2001AU-0004919.
17-DEC-2001; 2001AU-0009567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2002; 2002WO-AU00582
                                                                                02-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chopin LK, Jeffery PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-111957/10.
N-PSDB; AAD50726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AA;
                                                                                                                                                                                                                                                                                                    WO200290387-A1
                                                                                                                                                                                                breast; cervica
cancer; human.
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Gaps

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Homo sapiens

AAB60517;

RESULT 8 AAB6051

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Seguence

us-09-853-253-5.oli.rag

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AAZ98109 to AAZ98242 encode AAY87224 to AAX87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma. Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic an be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapeutics, for detecting related sequences criplex-forming or ribozyme therapeutics, for detecting related sequences criplex-forming or ribozyme therapeutic agents), Ab are used to diagnose, or antagonists (potential therapeutic agents), Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                            3A, Corley NC, Guegler KJ, Baughn MR;
Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 168-169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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                                                                                                                                                                                                                                                                            Gorgone GA,
                                                                                                                         98US-0102686.
98US-0102686.
98US-0112129.
                                                   99WO-US14484
                                                                                                    98US-0090762
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                                                                                                                                                                                                                                                                                                 Au-Young J,
                                                                                                                                                                                                                              PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-160673/14.
N-PSDB; AAZ98121.
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Matches 23; Conserv
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                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                              (INCY-) INCYTE
                                                                                                                                                                                                                                                                                                      Akerblom IE,
                                                   25-JUN-1999;
                                                                                                                                                   01-0CT-1998;
11-DEC-1998;
                                                                                                    26-JUN-1998;
                                                                                                                              31-JUL-1998;
06-JAN-2000
                                                                                                                                                                                                                                                                                                                             3andman 0;
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                                                                                                                                                                                                                                                                            Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a protein designated Zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or alielite variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zig33 agonists, antagonists and ligands and to produce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psorlasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 20;
100.0%; Pred. No. 2.3e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                  98WO-US05620
                                                                                                                                                                       97US-0041102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                            Sheppard PO;
                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                        WPI; 1999-070071/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX04550
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  WO9842840-A1
                                                                                                  23-MAR-1998;
                                                                                                                                                   24-MAR-1997;
                                                                                                                                                                       24-MAR-1997;
                                                                                                                                                                                                                                                                            Deisher TA,
                                                 01-OCT-1998
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Sequence

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Gaps

AAY87236;

RESULT 10 AAY87236

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receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 contacting the receptor with a zsig33 peptide (comprising residues 24-37 contacting the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for method is useful for purifying cells, purifying a receptor. It is also useful for method contractility, nutrient uptake, secretion of digestive and parcreatic enzymes and hormones, secretion of insulin-like growth factor. It secretion of non-zsig33 proteins. It is useful for modulating growth commone secretion in a mammal having a disease associated with abnormal commones of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, skeletal dysplasia, immune suppression, obesity, growth retardation, dareful disorder requiring neutropathy associated dareful disorder requiring neutropathy associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the human zsig33 release in a mammal. The present expresents the human zsig33 polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R.
 zsig33; signal transduction; hormone; enzyme; neural development; gastric contractility; nutrient uptake; digestive; pancreatic; human; insulin-like growth factor-1; growth hormone; bone; gastrointestinal; glucose; osteopethic; anorectic; vulnerary; immunomodulator; GHS-R:
                                                                                                                                                                     /note- "specifically claimed fragment that binds to the GHS-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of forming a reversible peptide
                                                                                                                                                                                                                                                                                                                                                                                               Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 22;
ilarity 100.0%; Pred. No. 2.3e-14;
Conservative 0; Mismatches 0;
                                                                                                                                   Location/Qualifiers 24..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 93-94; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ALAGWLRPEDGGQAEGAEDELEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20101 standard; Protein; 117
                                                                                                                                                                                                                                                                                           2000WO-US32074.
                                                                                                                                                                                                                                                                                                                           99US-0166765.
                                                                   G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                               Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                           (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-355879/37.
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es 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF83678
                                                                                                                                                                                                                         W0200138355-A2
                                                                                                                                                                                                                                                                                                                                                                                               Sheppard PO,
                                                                                                                                                                                                                                                                                           22-NOV-2000;
                                                                                                       Homo saptens
                                                                                                                                                                                                                                                                                                                           22-NOV-1999;
                                                                                                                                                                                                                                                         31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB20101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                         Key
Peptide
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Matches
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ID AAB2
XX
AC AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, incupaths and central nervous system diseases, such as localised neuropathses and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and thrombolytic activity, arthritis and inflammation, leukaemias and constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                             Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
2.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                         Chen R, Ma Y, (Xu C, Xue AJ, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 2035; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB Pred. No. 2.3(); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALAGWLRPEDGGQAEGAEDELEV 23
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100.0%;
                                                                                                                                                                                                    2000US-048B725.
2000US-0552317.
2000US-0598042.
                                                                                                                                                                                                                                                     2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                       2000US-0727344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.(
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human zsig33 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47
N-PSDB; AAI58046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEO INC.
                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification
                                                                                                                                                                                                                                  09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                       29-NOV-2000;
                                                                                                                                                                                                     21-JAN-2000;
                                                                                                                                                                                                                       -APR-2000
                                                                                                                                   26-JUL-2001
                                 leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                             OA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                           rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao
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Gaps

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Length 117; Indels œ

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The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghretlin homologues and are concentration in cells. The peptides are ghretlin homologues and are concentration a cid and/or a non-amino acid has been substituted by a modified amino acid and/or a non-amino acid has been substituted by a chormpasses the unmodified peptides; the DNA encoding the peptides vectors and host cells comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the peptides consed by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents a ghrift in the invention are safe with an accompanying side effects. The present sequence represents a constitution of the invention are safe with the invention are safe with the followed processing and the invention are safe with the followed processing and the invention are safe with the followed processing and the present sequence represents a constitution and the present sequence represents and the present processing and the present processing the processing and the present processing 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis
                           Growth hormone secretagogue, GHS; ghrelin; precursor; preproprotein; calcium concentration elevation; infant growth disorder; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoda H, Matsuo H, Minamitake Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Short gastrointestinal peptide; SGIP; zsig33; motilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 22; 100.0%; Pred. No. 2.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a human zsig33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALAGWLRPEDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 182; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of infant growth disorders -
                                                                                                                                                                                                                                                                                                                                                                        29-NOV-1999; 99JP-0338841.
26-APR-2000; 2000JP-0126623.
                                                                                                                                                                                                                                                                                           24-JUL-2000; 2000WO-JP04907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kangawa K, Kojima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-159704/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KANG/) KANGAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF59645
                                                                                                                                                                                    40200107475-A1
                                                                                                                                                                                                                                                                                                                                               23-JUL-1999;
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB78319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB78319
        Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of zsig33, a secreted protein with homology to motilin (see AAB20102). Zsig33 is expressed at high levels in the stomach, and at lower levels in the small intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP is a ligand for growth hormone secretagogue receptor, and is therefore useful for modulating secretion of growth hormone and insulin like growth factor 1 SGIP, and variant SGIP peptides, are used in claimed methods for stimulating contractability in duodenum or jejunum tissue,
                                                                                                     SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C; nutritional absorption modulator; growth hormone secretagogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variants of SGIP peptides for modulating contractility in duodenum or jejunum tissue, pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulating pancreatic secretion of hormones and digestive enzymes, inducing growth hormone secretion, and modulating gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      - SGIP_peptide
"this peptide is claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 22; Best Local Similarity 100.0%; Pred. No. 2.3e-14; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ghrelin preproprotein, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                        'label- Mature_protein
                                                                                                                                                                                                                                                                                                                       label- Signal_peptide
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAGWLRPEDGGQAEGAEDELEV 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0345157
(first entry)
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/label- S
/note- "t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF30033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastric emptying
                                                                                                                                                           therapy; human.
                                                   Zsig33 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200100830-A1
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1999;
23-APR-2001
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                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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AAB60511
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Length 117;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                New Short Gastrointestinal Peptide, which has homology to motilin, useful for preventing, diagnosing and treating gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 23; DB 23; Length 117; Best Local Similarity 100.0%; Pred. No. 2.3e-14; Matches 23; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                Deisher TA, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Columns 39-40; 23pp; English.
                    1..23
/note= "signal peptide"
24..119
/note= "mature protein"
Location/Qualifiers
                                                                                                                                                                                                         99US-141592P.
                                                                                                                                                                         30-JUN-2000; 2000US-0608B10.
                                                                                                                                                                                                                                                                               Sheppard PO, Jaspers SR,
                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                               WPI; 2002-634794/68.
N-PSDB; ABV72214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                           30-JUN-1999;
                                                                                                     US6420521-B1
                                                                                                                                      16-JUL-2002
   Key
Peptide
                                                    Protein
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1 ALAGWLRPEDGGQAEGAEDELEV 23

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Q90p76 human immun Q90p77 human immun Q9xsp0 capra hircu Q9xsp0 capra hircu Q9rsp0 capra hircu Q9rsp0 capra hircu Q9rsp17 human immun Q9np55 human immun Q8ru5 chimpanzee Q93vb3 oryza sativ Q9rby2 pseudomonas Q9cm8 pseudomonas Q9cm8 pseudomonas Q9cm8 pseudomonas Q9cm9 human immun Q90nl3 human immun Q90nl6 human immun Q90nl1 human immun
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090p37 human 1
094314 oryza s
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Homo sapiens (Human).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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090n19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC02791; AAH25791.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
SEQUENCE 117 AA; 12929 WW; 25B0572EBECB7610 CRC64;
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Last annotation update)
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Q8LRD5
Q9XSP0
Q9GLE4
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080RU5
093VB3
09RBY2
09R2S2
09R2S2
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090NL6
090NL0
090NL1
090NM1
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Q78494
Q90P53
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Q90P55
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08CH53;
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
    PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
  Local Similarity
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\begin{array}{c} \mathbf{4} \\ \mathbf{6} \\ \mathbf{
  Query Match
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Q8CH53
ID Q8CH1
AC Q8CH1
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Q8th53 meriones un
Q81415 plasmodium
Q91445 plasmodium
Q81016 oryza sativ
Q7774 plasmodium
Q20p58 human immun
Q20p50 human immun
Q90f101 pseudomonas
Q82036 hirame rhab
Q94189 hirame rhab
Q95169 capra hircu
Q95169 capra hircu
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Q90nl5 human immun
Q8ufa5 agrobacteri
                                                                                                                                                  September 11, 2003, 17:21:03; Search time 22.8449 Seconds (without alignments) 271.100 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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QB1573
QDU445
QBLNL6
Q90P58
Q27724
Q27724
Q816L1
Q82036
Q916L1
Q82036
Q91619
Q91638
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Q91638
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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sp_unclassified:*
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sp_bacteria:*
sp_fung1:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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126
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Plasmodium falciparum
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                                         NCBI_TaxID-5833;
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                                                                                                       East J.M.;
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Q8LNL6;
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                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                    Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
                                                                                                                                           "Nucleotide sequence of the Mongolian gerbil preproghrelin mRNA."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR442491; AA006695.1; -
SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
                       Meriones ungulculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.8%; Score 59; DB 5; Length 1208; llarity 52.6%; Pred. No. 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 419:498-511(2002).
EMBL; AE014846; AAN36207.1; -.
SEQUENCE 1208 AA; 133873 MW; 25AA7752E707E621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                        77.0%; Score 97; DB 11;
75.0%; Pred. No. 2.6e-06;
tive 2; Mismatches 4;
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STRAIN-3D7;
MEDLINE-22255705; PubMed-12368864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1072 GWCRPKDNKTSDGYNDELE 1090
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                                                                                                                                                                                                                      Best Local Similarity 75.0 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    P-type ATPase, putative.
PFL0590C.
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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               Ghrelin preproprotein.
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es 10; Conserv
                                                                                                      SEQUENCE FROM N.A.
                                                                           NCBI_TaxID-10047;
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090445;
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Matches
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Q815T3
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                                                                                                                                                                                                     'Expression and Functional Characterization of a Plasmodium falciparum
                                                                                                                                                                                                                                                                                      J. Biol. Chem. 276:10782-10787(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Nipponbare;
McComble W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
McComble W.R., Spiegel L., Zutavern T., Balija V., Ball M., Baker J.,
Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBa0071120, from chromosome 10, complete sequence.";
Submitted (JUL-2002) to the BNBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                    Ca2+-ATPase (PfATP4) Belonging to a Subclass Unique to Apicomplexan
                                                                                   SEQUENCE FROM N.A.
MEDLINE-21179120; PubMed-11145964;
Krishna S., Woodrow C., Webb R., Penny J., Takeyasu K., Kimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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1264 AA; 140261 MW; 638142BB1B433640 CRC64
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SEOUENCE 183 AA; 20492 MW; DE73BD8607292D7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.8%; Score 59; DB 5
Best Local Similarity 52.6%; Pred. No. 9.4;
Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRPAMS; TIGRO1494; APPASE_P-type; 5.
PROSITE; PSO0154; ATPASE_E1_E2; 1.
ATP-binding; Hydrolase; Phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR006068; Cation_ATPase_C.
InterPro, IPR004014; Cation_ATPase_N.
InterPro, IPR005834; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00689; Cation_ATPase_C; 1.
Pfam; PF00690; Cation_ATPase_N; 1.
Pfam; PF00122; E1-E2_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF203980; AAF17245.1; -.
HSSP; P04191; LBUL.
HCSPPro; IPR001757; ATPRSe_E1-E2.
InterPro; IPR006068; Cation_ATPRSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1128 GWCRPKDNKTSDGYNDELE 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GWLRPEDGGQAEGAEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 47.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 10; Conserv
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A persistent Reservoir for HIV-1 in Alveolar Macrophages.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ARTO019; AAK66318.1; -.
Interpro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.3%; Score 52; DB 15; Length 201; Best Local Similarity 45.5%; Pred. No. 14; Matches 10; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                     Score 53; DB 5; Length 1228;
Pred. No. 66;
3; Mismatches 6; Indels
                                                       TIGRFAMS; TIGR01494; ATPase_P-type; 5.
PROSTIE; PS00154; ATPASE_BL_E2; 1.
ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SEQUENCE 1228 AA; 135989 MW; 32C3CFD324964CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6CAF6C460A9BA517 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 AA.
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01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · PRT;
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                                                                                                                                                                                                                                                                                                                                                               1131 WCRPKDNKTSDGYNDELE 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Envelope glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                                          5 WLRPEDGGQAEGAEDELE 22
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                                                                                                                                                                                                           42.1%;
50.0%;
PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0°
Matches 9; Conservative
                              HATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                              PRINTS; PR00120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nickle D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090P50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A Persistent Reservoir for HIV-1 in Alveolar Macrophages.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR70011; AAK66310.1; -.
InterPro; IPR00077; GP120.
Pfam: PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.1%; Score 53; DB 15; Length 202; llarity 45.5%; Pred. No. 9.9; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 202
202 AA: 22572 MW; 4CB8ACAFBFB14314 CRC64;
                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Envelope glycoprotein (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID-11676;
                                                                                                                                                                                                                                      202 AA.
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InterPro: IPR004014; Cation_ATPase_N.
InterPro: IPR005934; Hydrolase.
InterPro: IPR00695; H_ATPase.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2003 (TEMBLrel. 23, Last anno
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                                                                                                                                                                                                                                      PRT;
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EMBL, U39298; AAC47167.1; -.
HSSP; P04191; 1EUL.
InterPro; IPR001757; ATPASe_E1-E2.
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Pfam; PF00690; Cation_ATPase_N; 1.
PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; HydroLase; 1.
                           3 AGWLRPEDGGQAEGAEDELEV 23
                                                             53 AGWIETEDGSDEESDESDSEV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96408665; PubMed-8813672;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFATPASE4.
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-type ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nickle D.C.;
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NON_TER
SEQUENCE
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Best Local 9
                                                                                                                                                                                                                                                               090P58;
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InterPro; IPR004902; Rhabdo_ncap_2.
Pfam; PF03216; Rhabdo_ncap_2; 1.
SEQUENCE 392 Aa; 42465 MW; C5A282238FC7A638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                       Query Match
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Q9N638;
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Q95169
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                 opportunistic pathogen.";
Nature 406:959-964(2000).

Rature 406:959-964(2000).

REGULATORS.

EMBL, AROUA466, AAG03668.1; -

InterPro; IPR01845; HTH_ArsR.

PRINTS; PR00778; HTH_ARSR.

PRINTS; SM00418; HTH_ARSR.

SMART; SM00418; HTH_ARSR.

SMART; SM00418; HTH_ARSR.

SMART; SM00418; HTH_ARSR.

SMART; SM00418; HTH_ARSR.

SEQUENCE 232 As; 24440 MW; E3C29187694CF936 CRC64;
                                                                                                                                                                                                                                                                               Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 249;
  "Complete genome sequence of Pseudomonas aeruqinosa PAO1,
                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;
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STRAIN=CA 9703;
Oh H.K., Chol T.J.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104985; AAF14116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases. EMBL: D45422; BAA08261.1; ...
InterPro: IPRO04902; Rhabd_c.ncap_2.
Pfam; PF0316; Rhabd_c.ncap_2; 1.
SEQUENCE 249 AA; 26936 WW; 62FF2BFA5D47DB89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                               Score 52; DB 16;
Pred. No. 16;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.3%; Score 52; DB 12; 75.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 AA
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                                                                                                                                                                                                                                                                               41.3%;
72.7%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-UNW-2002 (TrEMBLrel. 21,
Nucleocapsid protein.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             11111:11 :1
202 GWLRPQDGSRA 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 EDGGQAEGAEDE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     4 GWLRPEDGGQA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirame rhabdovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishizawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q82036
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Q9QL89
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                                        Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Boyidae, Caprinae, Capra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-37008165; Pubmed-8855341;
Beck C.L., Fahlke C., George A.L.;
"Molecular basis for decreased muscle chloride conductance in the
                                                                                                                                                                                                                                                                                                                              Skeletal muscle voltage-gated chloride channel gClC-1 (Fragment).
Capra hircus (Goat).
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41.3%; Score 52; DB 12; Length 392;
75.0%; Pred. No. 28;
Live 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilkinson J.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 1
SEQUENCE 977 AA; 107894 MW; 1E462B3CB307A148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myotonic goat.";
Proc. Natl. Acad. Sci. U.S.A. 93:11248-11252(1996).
EMBL; U60275; AAC48666.1;
InterPro; IPR001647; CBS. domain.
InterPro; IPR001807; Cl-Channel_volt.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00571; CBS; ZB.
Pfam; PF00571; CBS; ZB.
PRINTS; PR00762; CLCHANNEL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                        O95169 PRELIMINARY; PRT; 977 AA. 05169; C15169; C1FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0LMAR-2003 (TrEMBLrel. 23, Last annotation update)
F37D6.6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.3%; Score 52; DB 62.5%; Pred. No. 73;
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                                                                                                          1111: [1 | 1 | 378 EDGGEGEGGEDE 389
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                                          Conservative
                                                                                9 EDGGQAEGAEDE 20
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                     Best Local Similarity
Aatches 9; Conservat
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SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Raistoniaceae; Raistonia.
                                                                                                                                                                                                       Score 51.5; DB 5; Length 436; Pred. No. 37; 5; Mismatches 2; Indels
                                                        MCMURTRY A.A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 27540; CAB70221.1; JOINED.
EMBL; 275540; CAB70215.1; -..
EMBL; 275010; JOINED.
MormPep; F7700.6; CE24960.
InterPro; IRR003132; Dwarfin.A.
Ffam; PF03166; MI2; 1.
FMART; SM00523; DWA: 1.
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         'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                   49496 MW; EOC71263BC580EEE CRC64;
                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein RSc2585.
RSC2585 OR RS00797.
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9
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58.8%; Pred. No. 15;
tive 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                       158 AA.
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                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-21681879; PubMed-11823852;
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169 WIRPETNGGDDDGSEDK 185
                                                                                                                                                                                                                                                5 WLRPE-DGGQAEGAEDE 20
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                                                                                                                                                                                                       40.9%;
52.9%;
                   investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                      Query Match
Best Local Similarity 52.99
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                    436 AA;
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Matches 10; Conserv
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SEQUENCE FROM N.A.
                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                    SEQUENCE
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090NL5;
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Q90NL5
ID Q90NL
AC Q90NL
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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September 11, 2003, 17:21:03 ; Search time 3.46524 Seconds
(without alignments)
325.703 Million cell updates/sec Run on:

US-09-853-253-4

1 ALAGWLRPEDGGQAEGAEDELEVR Perfect score: Sequence:

24

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CHMMADIEC

	otion	homo sapien	rattus norv	sus scrofa	mus musculu	bos taurus	canis famil	xenopus lae	bacillus su	mus musculu	bison bison	bos taurus	methanopyru	homo sapien		-		agrobacteri		homo sapien	mus musculu	rattus norv	homo sapien	schizosacch		escherichia	homo sapien	deinococcus	oryctolagus	homo sapien	homo sapien	vicia faba	homo sapien	reovirus (t
	Description	Enqn60	Q9qyh7	09gky5	08edx0	09bdj6	09bef8	P05221	035031	003157	046383	028139	Q8tx28	P05019	P41144	038953	P15718	Q8ufa2	Q9xt90	P50281	P53690	010739	P49023	009757	002516	P25905	09h3m0	09ru23	P16230	P29376	092543	043876	015211	P15024
ro.																																		
SUMMARIES	ΩI	GHRL_HUMAN	GHRL_RAT	GHRL_PIG	GHRL_MOUSE	GHRL_BOVIN	GHRL_CANFA	NUPL_XENLA	ACYP_BACSU	APP1_MOUSE	NKX1_BISBI	NKX1_BOVIN	SYM_METKA	IGFB_HUMAN	OPRK_CAVPO	DDX8_ARATH	POLB_MAIZE	SYM_AGRT5	MM14_PIG	MM14_HUMAN	MM14_MOUSE	MM14_RAT	PAXI_HUMAN	RS9A_SCHPO	HAP5_YEAST	WZZE_ECOLI	KCF1_HUMAN	PYRG_DEIRA	SRCH_RABIT	KLTK_HUMAN	SNXJ_HUMAN	SPS_VICFA	RGL2_HUMAN	VL1_REOVD
	DB	-	-	-	-	_	-	-	-	-	-	-	-		ч	-	-	٦	-	-	-	-	-		-	_	-	-	-	-	-		1	
	Ouery Match Length	117	117	118	117	116	117	200	91	653	300	1216	668	195	380	1168	740	516	580	582	582	582	591	190	242	349	464	544	852	864	992	1059	777	1233
æ	Query	100.0	75.4	73.0	72.2		-:	42.9	40.5	39.7	38.9	38.9	38.1	37.7	37.3		36.9	36.5	36.1	36.1	36.1	36.1	36.1		35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.3	35.3
	Score	126	95	92	91	77	73	54	51	20	49	49	48	47.5	47	4	46.5	**	45.5	ς.	'n.	S.	•	45	45	45		45	4.5	<b>4</b>	45	45	44.5	44.5
	Result No.	н	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

Q9w7r2 verasper mo Q944w6 brassica ol	P42586 mus musculu Q8v1g3 mus musculu P05059 bos taurus	P40803 bacillus su Q9rxel deinococcus	Q95220 oryctolagus O43709 homo sapien Q9d5v6 mus musculu	P41145 homo sapien Q8pnz5 xanthomonas
INS_VERMO TCTP_BRAOL	NK22_MOUSE TSA2_MOUSE CMGA_BOVIN	PKSK_BACSU SYK_DEIRA	MM14_RABIT WS22_HUMAN SYAP_MOUSE	OPRK_HUMAN SYQ_XANAC
115 168	273 301 449	525	582 281 365	380 579
34.9	34.9 34.9	34.9	34.5 34.1	34.1 34.1
4 4 4 4	7 7 7 7 7 7	44	43.5 43.5 43.5	443
34 35	36 37 38	39	4 4 4 4 4 4 4 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44 45

## ALIGNMENTS

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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

K Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

K Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

K Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

K Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

K Rhards S. Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

K Willalon D.K., Mazup D.M., Sodergren E.J., Lu X., Gibbs R.A.,

K Willing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
MEDLINE-20067959; Pubmed-10064470,
KOjima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            Q9UBU3; Q8TAT9; Q9H3R3; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42 annotation update) Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomesetto C., Karam S.M., Rio M.-C.;
"Identification of a novel gastric protein m46.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L.; "Genomic organization of the human Ghrelin gene."; J. Endocrinol. Genet. 1:231-233(2000).
                                                                            A.
                                                                            117
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                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:656-660(1999).
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                          GHRL OR MTLRE
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                                                                            GHRL_HUMAN
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                                        GHRL_HUMAN
RESULT 1
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Length 117;

100.08;

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117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
                                                                              Local Similarity
                                                                                                          24;
SEQUENCE
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Name-1; Synonyma-Ghrelin;
Isoid-Ogubu3-1; Sequence-Displayed;
Name-2; Synonyma-del-Gln14-ghrelin;
Isoid-Ogubu3-2; Sequence-VSP_00345;
PTM: Orn-octanoylation is essential for activity.
PTM: Orn-octanoylation is essential for activity.
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/GhreliniD327.html".
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R GO; GO:0005615; C:soluble fraction; TAS.
R GO; GO:0005615; C:soluble fraction; TAS.
R GO; GO:0007267; P:cell-cell signaling; TAS.
R GO; GO:0007186; P:cell-cell signaling; TAS.
R InterPro; IPR006738; motilin_assoc.
R InterPro; IPR006738; motilin_assoc.
R Pfam; PF04644; motilin_assoc.
R Pfam; PF04644; motilin_assoc.
R PRINTS; PR01624; GHREIIN.
R PRINTS; PR01624; GHREIIN.
R PRODOm; PD332162; Preproghrelin; 1.
R PRODOm; PD332162; Preproghrelin; 1.
R PLEMATIVE SPICETOR PASIC PREPROMENTING; PR01624; MAITERNATIVE SPICETOR PASIC PREPROMENTING; PR01624; MAITERNATIVE SPICETOR PASIC PREPROMENTING; PASIC PROMENTING; PASIC PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21203998; PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                       Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.; "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; Gastroenterology 119:395-405(2000).
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Missing (in isoform 2).
/FTId=VSP_003245.
L -> M (IN REF. 5).
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                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                             TISSUE-Stomach;
MEDLINE-20389976; Pubmed-10930375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ252278; CAB67331; -. EMBL; AF29658; AAG10300.1; -. EMBL; BC025791; AAH25791.1; -. PIR; A59316; A59316.
                                                  and mouse cDNA sequences.
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117
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                                                                                                                                 SEQUENCE OF 24-33.
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VARSPLIC
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"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Structure-activity relationship of ghrelin: pharmacological study of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY
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Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
"Ghrelin is a growth-hormone-releasing acylated peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Specific ligand for the growth hormone secretagogue
receptor type 1 (GHSR) inducing the release of growth hormone
the pituitary. Has an appetite-stimulating effect, induces
adiposity and stimulates gastric acid secretion. Involved in
growth regulation.
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STRAIN-Sprague-Dawley; TISSUE-Stomach;
MEDLINE-20357315; Pubmad=10801861;
Hosoda H., Kojima M., Matsuo H., Kangawa K.;
PurIfication and characterization of rat des-Gin14-ghrelin, a see endogenous ligand for the growth hormone secretagogue receptor."; J. Biol. Chem. 275:21995-22000(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        Q9QY#7; Q9ET69;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
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                                                                   Indels
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Score 126; DB 1;
Pred. No. 3.8e-11;
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                                                                                                                                                                                                                                                                                                                                                                        117 AA.
                                                                   Mismatches
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                                                                                                                                                                    52 ALAGWLRPEDGGQAEGAEDELEVR 75
                                                                                                                                    1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                            100.0%;
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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AND ACYLATION OF SER-26.
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GHRL_MOUSE
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              Name=1; Sylucyms=-our-time; Isold=-090YH7-1; Sequence=Displayed; Name=2; Sylucyms=-del-Gln14-ghrelin; Isold=-090YH7-1; Sequence=VSP_-00348; Isold=-090YH7-2; Sequence=VSP_-00348; Isold=-090YH7-2; Sequence=VSP_-00348; Isold=-our-time; Isold=-our-
                                                                                                                                                                                                                                                                                                             -1- MASS SPECTROMETRY: MW-3187.1; MW_ERR-0.6; METHOD-Electrospray;
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Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHRL_PIG STANDARD; PRT; 118 AA.
09GKY25, 09BDGS; 09GKY4.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
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/FTId=VSP_003248.
8857546FE51A7691 CRC64;
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-!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
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2; Mismatches
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InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
PRINTS; PR01624; GHRELIN.
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Synonyms-Ghrelin;
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Matches 18; Conservative
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                                                                                                                                                                                                                                                        -! - MASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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Rousselle J., Lacroix D., Dubreuil P.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNTION: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, Induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=Chrelin;
IsoId=Q9GKY5-1; Sequence=Displayed;
IsoId=Q9GKY5-2; Sequence=USP=00347;
IsoId=Q9GKY5-2; Sequence=VSP=00347;
PTM: O-n-coctanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMOVED IN MATURE FORM (BY SIMILARITY).

N-OCTANOATE (BY SIMILARITY).

Missing (in 1soform 2).

FYIId-VSP_00324.

L -> P (IN REF. 2; AAK30002).

K -> E (IN REF. 2; AAK30002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
Pfam; PF04644; GHRELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide) (Motilin-related peptide) (M46 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856D3E1D6DAB1A76 CRC64;
                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92; DB 1;
Pred. No. 2.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB035704; BAB19049.1; -.
EMBL; AF308930; AAK19243.1; -.
EMBL; AY028942; AAK30002.1; -.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR006741; preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALAGWLRPEDGGQAEGAEDELEVR 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12785 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7'
Matches 16; Conservative
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ACCENTE TOWN NO. 1. (1500 PM 1).

STAIN-CSTBL/63; TISSUB-Stomach.

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Lawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Lawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Saludi R., Kochiwa H.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Romstein M.J., Bult C., Fletcher C., Fullita M., Mombaerts P.,

Romostein M.J., Bult C., Fletcher C., Fulliya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Rymshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanahizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21203998; PubMed-11306336;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
Kojima M., Hosoda H., Matsuo H., Kangawa K.;
Ghrelin: discovery of the natural endogenous ligand for the growth hormone secretagogue receptor.";
Trends Endocrinol. Metab. 12:118-122(2001).
-!-FUNCTIONS: Specific ligand for the growth hormone secretagogue receptor type I (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces.
adiposity and stimulates gastric acid secretion. Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event-Allernative splicing; Named isoforms-2;
Name=1; Synonyms-Ghrelin;
Isold-09EQX0-1; Sequence-Displayed;
Isold-09EQX0-2; Sequence-VSP_003246;
Isold-09EQX0-2; Sequence-VSP_003246;
TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract with higher levels in the stomach, medium levels in the doodenum, jejunum ileum and colon. Low expression in the testis and brain.
Not detected in the salivary gland, pancreas, liver and lung.
FTM: O-n-octanoplation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1). Tanaka M., Nakai N., Nakashima K.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
TISSUE-Stomach;

MEDLINE-2038976: PubMed-10930375;

MEDLINE-2038976: PubMed-10930375;

Tomasetto CS., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.;

"Identification and characterization of a novel gastric peptide hormone: the motillin-related peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mouse mRNA for preproghrelin.";
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kojima M.
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                      ProDom; PD332162; Preproghrelin; 1. Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                     N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                      72.2%; Score 91; DB 1; Length 117
70.8%; Pred. No. 3.6e-06;
.ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              EACB49D2E3CA7203 CRC64;
                                                                                                                                                                                                                                                                                                                /FTId=VSP_003246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AA.
       EMBL, AJ243503; CAB46500.1; --
EMBL, AB035701; BAB19046.1; --
EMBL, AR008058; BAB25814.1; --
EMBL, AK008806; BAB25814.1; --
EMBL, AK008806; BAB25934.1; --
EMBL, AK008806; BAB25934.1; --
GO; MGI:1930008; Ghrl.
GO; CO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:cytoplasm; IDA.
InterPro; IPR006737; motilin_ghrelin.
InterPro; IPR006737; motilin_ghrelin.
Pfam; PF044643; motilin_assoc; 1.
Pfam; PF044643; motilin_assoc; 1.
Pfam; PF044643; motilin_assoc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHRL_BOVIN STANDARD; P 09BDJ6; Q9GKY6; 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                              117 AA; 13207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Query Match 72.2
Best Local Similarity 70.8
Matches 17; Conservative
                                                                                                                                                                                                                                Alternative splicing.
                                                                                                                                                                                                                                                           24
52
26
37
                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                             PEPTIDE
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AJ298296; CAC29156.1;
                                                                                                                                                         117 AA;
                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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52
26
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                                                                                                                                                                                                                                                                                                                                    Nucleoplasmin
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                                                                                                                                                                                                                                                                                    NUPL_XENLA
P05221;
                                                                                                                                                         SEQUENCE
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PROPEP
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                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms-2;
Name-1; Synonyms-Ghrelin;
IsoId-Q9BER8-1; Sequence-Displayed;
Name-2; Synonyms-del-Gln14-ghrelin;
IsoId-Q9BER8-2; Sequence-VSP_003244;
PTM: O-n-octanoylation is essential for activity (By similarity).
SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
                                                                                                                                                                                                        Gaps
                                                                                                                 BY SIMILARITY.
GHRELIN (BY SIMILARITY).
MACHOVED IN MATURE FORM (BY SIMILARITY).
N-OCTANOATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omasetto C., Wendling C., Rio M.-C., Poitras P.; Identification of cDNA encoding WTLRP/ghrelin precursor from dog
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                 PRINTS; PROJ624; GHELIN.
ProDom; PD332162; Preproghrelin; 1.
Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein
                                                                                                                                                                                                                                                                                                  09BEF8; 09BEF7;
28-FBF-2003 (Rel. 41, Created)
28-FBF-2003 (Rel. 41, Last sequence update)
15-FBF-2003 (Rel. 42, Last annotation update)
Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
                                                                                                                                                                                                        ;
0
                                                                                                                                                                                     Length 116;
                                                                                                                                                                   K -> E (IN REF. 2).
F55536DAC5FA59B6 CRC64;
                                                                                                                                                                                                                                                                                            117 AA.
                                                                                                                                                                                                      1; Mismatches
 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                 InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_ghrelin.
InterPro; IPR005441; Preproghrelin.
Pfam; PF04643; motilin_assoc; 1.
Pfam; PF04644; motilin_assoc; 1.
Pfam; PF04644; motilin_ghrelin; 1.
                                                                                                                                                                                                                         2 LAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                    EMBL; AF350329; AAK18612.1; -.
                             BAB19047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ298295; CAC29155.1; -.
                                                                                                                                                                116 AA; 12792 MW;
                                                                                                                                                                                   61.18;
69.68;
                                                                                                                                                                               Ouery Match
Best Local Similarity 69.67
Matches 16; Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Gastric fundus;
Tomasetto C., Wendling
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                             EMBL; AB035702;
                                                                                                                                                                                                                                                                                            GHRL_CANFA
                                                                                                                                                       CONFLICT
                                                                                                                                                                 SEQUENCE
                                                                                                                          PEPTIDE
PROPEP
                                                                                                                  SIGNAL
                                                                                                                                              LIPID
                                                                                                                                                                                                                                                                                 GHRL_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1ts developmental expression.";
Genes Dev. 1:97-107(1987).
-1-FUNCTION: NUCLEOPLASMIN IS AN ACIDIC, PENTAMERIC, THERMOSTABLE
PROTEIN WHICH IS ABLE TO ASSEMBLE NUCLEOSOMES BY BINDING HISTONES
AND TRANSFERRING THEM TO DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buerglin T.R., Mattaj I.W., Newmeyer D.D., Zeller R., de Robertis E.M.; "Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                              GHRELIN (BY SIMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
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                                                                                                                                                                                                    Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein; Alternative splicing.

1 23 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts an sluster of sequences homologous to putative nuclear localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dingwall C., Dilworth S.M., Black S.J., Kearsey S.E., Cox L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                     N-OCTANOATE (BY SIMILARITY). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3E57FED9D1847CF7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG-VSP_003244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
InterPro, IPR006737; motilin_assoc.
InterPro, IPR006738; motilin_ghrelin.
InterPro, IPR005441; Preproghrelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAGWLRPEDGGQAEGAEDELEVR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed froq)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                Pfam: PF04643; motilin_assoc; 1.
Pfam: PF04644; motilin_ghrelin; 1.
PRINTS: PR01664; GHRELIN
ProDom; PD332162; Preproghrelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88112783; PubMed-3428591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-87218476; Pubmed-2884102;
                                                                                                                                                                                                                                                                                                                                                                                                                                           13007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04766; CAA28460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 7-200 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 6:69-74(1987).
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Query Match
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     RRAPA RRAPA PRAPA 
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Braun M., Brignells S.C., Bron S.,
Brouillet S., Bruschl C.V., Caldwell B., Capuano V., Carter N.M.,
A Brouillet S., Bruschl C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
                                                                                                                                                                                                                                 HISTONE BINDING SITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 200; Pred. No. 1.1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A91DD110F2965812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Purative acylphosphatase (EC 3.6.1.7) (Acylphosphate
phosphohydrolase).
                                                                                                                                                                                                                                                                                D -> N (IN REF. 2).
E -> A (IN REF. 2).
N -> I (IN REF. 2).
N -> H (IN REF. 2).
A -> K (IN REF. 2).
T -> S (IN REF. 2).
T -> S (IN REF. 2).
L -> V (IN REF. 2).
C -> P (IN REF. 2).
C -> P (IN REF. 2).
                                                                                                                                                                                                                              (PROBABLE
                                               PDB; 1EE5; 26-SEP-01.
PDB; 1EJY; 24-APR-00.
PDB; 1K5J; 21-NOV-01.
InterPro; 1FR004301; Nucleoplasmin.
Pfam; PF03066; Nucleoplasmin; 1.
Nuclear protein; Phosphorylation; 3D-structure.
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-AC327;
MEDLINE-97417488; Pubmed-9272861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WLRPEDGGQAEGAEDELE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%;
55.6%;
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EMBL; Y00204; CAA68363.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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27
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les 10; Conserv
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035031;
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Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pulic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
Sakor T., Scanlan E., Schledth S., Schroeter R., Scoffone F.,
Schiguchi J., Sakowska A., Seroz S.J., Serror P., Shin B.S.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannider F., Vassarotti A.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Ryoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.;
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O = a fatty acid anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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003157; 08VC38;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanz1 R.E.,
Solomon F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.5%; Score 51; DB 1; Length 91; 44.0%; Pred. No. 1.4;
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PROSITE; PS00150; AcylphOSPHATASE_1; 1.
PROSITE; PS00151; AcylphOSPHATASE_2; 1.
HYPOTHELCAI profesh; Hydrolase; Complete proteome.
SEQUENCE 91 AA; 10318 MW; 50795631BF3310F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D86417; BAA22305.1; -.
EMBL; 299108; CAB12593.1; -.
ETR; B69811; B69811.
HSPP; P00818; 1APS.
Subtilist; BG12947; yflL.
InterPro; IPR001792; AGV1phosphatase.
Pfam.; PF00708; AGV1phosphatase.
Pram.; PR00708; AGV1phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LAGWLRPEDGGQ----AEGAEDELE 22
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Matches 11; Conserv
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Trocessing of beca-amytous precursor, the process.

The secretase regulates transcription.";

J. Biol. Chem. 277:44195-4420[2002].

The secretase regulates transcription.";

The secretase regulates transcription.";

The secretase regulates transcription.

The secretase processed fragment, ALIDI, activates transcription activation through APBB1 (Fee5) binding. Couples to JIP signal activation through APBB1 (Fee5) binding. May interact with activation through APBB1 (Fee5) binding. Couples to JIP signal collipsed to Signal activation through binding to components of the extracellular activation and papers and collagen I.

The secretase processed fragments of the extracellular matrix such as heparin and collagen I.

The secretase processed fragments of the extracellular matrix such as heparin and collagen I.

The secretase transcription of several collagents and APBB and APBB and APBB and APBB family members, warkfalls and APBB and APBB and APBB family its its
                                                                                         Straubberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A slighten M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Rownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Robas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Nathing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Samilus D.E.,
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96139497; PubMed-8576160; Beher D., Hesse L., Masters C.L., Multhaup G.; Beher D., Gamylold protein precursor (APP) binding to collagen and mapping of the binding sites on APP and collagen type I."; J. Biol. Chem. 271:1613-1620(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH DAB1.
MEDLINE-99389880; PubMed-10460257;
Homayouni R., Rice D.S., Sheldon M., Curran T.;
"Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22313598; Pubmed-12228233;
Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.;
"Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIANE-21408156; PubMed-11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T., Hatsul S., Yasukawa T., Homma Y., Ito Y., Niikura T., Haraki T., Ahno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.; "C-jun N-terminal kinase (JNK)-interacting protein-lb/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine phosphorylation.
SUBCELLULAR LOCATION: Type I membrane protein. C-terminally processed in the Golgi complex.
DOMAIN: The NPXY sequence motif found in many tyrosine-
                                                                       MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurosci. 19:7507-7515(1999).
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                                                                                -!- PTM: N-glycosylated.
-!- PTM: O-glycosylated.
-!- PTM: O-glycosylated.
-!- MISCBLIANROUS: Binds zinc and copper in the extracellular domain.
Zinc-binding increases heparin binding. No Cu(II) reducing activity with copper-binding.
-!- SIMILARITY: BELONGS TO THE APP FAMILY.
terminal to the NPXY motif are often required for complete interaction. The NPXY site is also involved in clatherin-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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PROSITE; PS00320; A4_INTRA; 1.
Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
Heparin-binding; Metal-binding; Copper; 2inc; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REQUIRED FOR COPPER(II) REDUCTION (BY
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINED (GLCNAC. . .) (POTENTIAL).
Y->G: REDUCED BINDING OF APBBI.
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ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
                                         PTM: Proteolytically cleaved by caspases during neuronal apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARIII).
BASOLATERAL SORTING SIGNAL (BY
SIMILARIIY).
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56516DC3EA40E4B0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMYLOID-LIKE PROTEIN 1. C30 (BY SIMILARITY).
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1; Mismatches
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EMBL; BC021877; AAR21877.1; -.
PIR; A46362; A46362
HSSP; P05067; 1MWP.
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76.98;
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InterPro; IPR001868; A4_APP.
Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00006; A4_EXTRA; 1.
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Best Local Similarity 76.9
Matches 10; Conservative
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653 AA;
                              endocytosis.
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CONFLICT
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RESULT 10 NKX1_BISBI

phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-

(ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;

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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with a revised bovine sequence.",
Invest. Ophthalmol. vis. Sci. 39:435-440(1998).

- FUNCTION: Critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and cone photoreceptors and the light-induced lowering of calcium is caused by extrusion via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+) (By similarity).

- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98138491; PubMed-9478004;
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
"cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                          Bison bison (American bison).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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2878139; 046384;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Resting annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-
exchange prottein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vision; Transport; Antiport; Symport; Calcium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31671 MW; 2BE592DA5AB9781E CRC64;
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300 AA
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   STANDARD;
                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bison.
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300
300 AA;
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                                                                                                                                                                                                     SLC24A1 OR NCKX1
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9901;
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NKX1_BISBI
046383;
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                                                                                                                  "Primary structure and functional expression of the Na/Ca,K-exchanger from bovine rod photoreceptors."; EMBO J. 11:1689-1695(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vision; Transport; Antiport; Symport; Calcium transport;
Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
Phosphorylation; Signal; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
                                                                         Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note-No experimental confirmation available;
TISSUE SPECIFICITY: Retina.
SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                           SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-Q28139-2; Sequence-VSP_006159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId-Q28139-1; Sequence-Displayed;
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PIR; S20969; S20969.
InterPro; IPR004817; K_NaCaexchang.
InterPro; IPR004837; NaCa_Exmemb.
Pfan; PF01699; Na_Ca_Ex; Z.
TIGREAMS; TIGR00367; ZA1904; 1.
                                              MEDLINE-92258377; PubMed-1582405;
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647-660 AND 1119-1136.
                    TISSUE-Retina;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license else-entities commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  EMBL; AE010375; AAM02063.1; -.

R HAMAP; MF_00098; fused; 1.

R InterPro; IPR004295; MeCfcterm.

R InterPro; IPR001412; tRNA-synt_1.

R InterPro; IPR002304; tRNA-synt_1.

R InterPro; IPR002547; tRNA-synt_1.

R InterPro; IPR002547; tRNA-synt_1.

R Ffam; PP0133; tRNA-synt_1.

P Fam; PP01389; tRNA-synt_1.

R FIRSP; PIRSF001589; MetRs_dimertsing; 1.

R TICRFAMS; TICR00399; metCc_term; 1.

PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

R PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

R PROSITE; PS00186; TRND; 1.

Aminoacy1-tRNA synthetase; Protein blosynthesis; Ligase; ATP-binding; KNA-binding; tRNA-binding; Metal-binding; 2inc; Complete proteome.

FT SITE 332 336 "KMSKS" REGION.
                                                                   SIMILARITY: Contains 1 tRNA-binding domain.
                 SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family. MetG subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-80168194; PubMed-2937782;
Rotwein P., Pollock K.M., Didier D.K., Krivi G.G.;
"Organization and sequence of the human insulin-like growth factor
gene. Alternative RNA processing produces two insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SIA (Rel. 42, Last annotation update)
16F1 ON 1BP1.
16F1 ON 1BP1.
16F2 ON 1BP1.
16F2 ON 1BP1.
16F3 ON 1BP1.
16F3 ON 1BP1.
17F3 ON 1BP1.
17F4 ON 1BP1.
17F4 ON 1BP1.
17F5 ON 1BP
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ZINC (BY SIMILARITY).
FBC5734FF5FEF015 CRC64;
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  SUBCELLULAR LOCATION: Cytoplasmic
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Biol. Chem. 261:4828-4832(1986)
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MEDLINE-86094355; Pubmed-3455760;
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15-SEP-2003 (Rel. 42, Last anno
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53.3%;
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547 LLPEESGESEGQDDE 561
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8; Conserva
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668 AA;
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P05019;
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Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
The complete genome of hyperthermophile Methanoprus kandleri AV19
The Complete genome of hyperthermophile Methanophile Hyperthermophile Methanophile Hyperthermophile Methanophile Hyperthermophile Methanophile Hyperthermophile Methanophile Hyperthermophile Methanophile Methano
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                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

8 X 17 AA TANDEM REPEATS OF D-E-G-E-I-Q-A-G-E-IG-I-G-B-V-[EK]-G.

1 (Q-A-G-E-IGTE).
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Archaea: Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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MASSING (in isoform 2).
/FTIG-VSP_006159.
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
MISSING (IN REF. 1; AA SEQUENCE).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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POLY-GLU.
PHOSPHORYLATION (POTENTIAL).
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39F149A74D1D0523 CRC64;
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                                                                                         POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                        EXTRACELLULAR (POTENTIAL)
                                                                CYTOPLASMIC (POTENTIAL).
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  POTENTIAL
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GEIQAGEGGEVEGDEDEGEIQ 836
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STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; Pubmed-11930014;
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Matches 9; Conserva+*****
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1216 AA; 131614
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SYM_METKA
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Raschdorf F., Dahinden R., Maerki W., Richter W.J., Merryweather J.P.; "Location of disulphide bonds in human insulinitike growth factors (16Fs) synthesized by recombinant DNA technology."; Blomed. Environ. Mass Spectrom. 16:3-8(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato A., Nishimura S., Ohkubo T., Kyogoku Y., Koyama S., Kobayashi M., Yasuda T., Kobayashi Y.; Tasuda T., Kobayashi M., Yasuda T., Kobayashi Y.; Tasuda T., Kobayashi M., Yasuda T., Kobayashi M., Kobayashi M., Yasuda T., Kobayashi M., Kobayashi M., Yasuda T., Kobayashi M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooke R.M., Harvey T.S., Campbell I.D.; "Solution structure of human insulin-like growth factor 1: a nuclear magnetic resonance and restrained molecular dynamics study."; Blochemistry 30:5484-5491(1991).
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MEDLINE-66108862; Pubmed-3002851;
MEDLINE-66108862; Pubmed-3002851;
MEDLINE-Holthuizen P., van Schaik F.M.A., Verduijn G.M.,
van Ommen G.J.B., Bound B.N., Jansen M., Sussenbach J.S.;
"Organization of the human genes for insulin-like growth factors I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 49-118.
MEDLINE=78130171; PubMed=632300;
Rinderknecht E., Humbel R.E.;
"The amino acid sequence of human insulin-like growth factor I and its structural homology with proinsulin.";
J. Biol. Chem. 253:2769-2776(1978).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 22-50 FROM N.A.
MEDLINE-84295593; PubMed-6382022;
Dull T.J., Gray A., Hayfilck J.S., Ullrich A.;
"Insulin-like growth factor II precursor gene organization in relation to insulin gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83210259; PubMed-6189745;
Blundell T.L., Bedarkar S., Humbel R.E.;
Tartiary structures, receptor binding, and antigenicity of
insulinilye growth factors.";
Fed. Proc. 42:2592-2597(1983).
human liver.";
Proc. Natl. Acad. Sci. U.S.A. 83:77-81(1986).
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MEDLINE-92316903; PubMed-1319992;
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                                                                                                                                                                                                                                                                                  FEBS Lett. 195:179-184(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS.
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   CCCGLABAAAKKIIIABAAAKKIKIIABAKAKKIKAAAKAAKAKKIIABKAAKAKKIIABKKAIABKAKKIIAAKKAKIIAKKAKAKAKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: 00:005199; F:insulin-like growth factor receptor binding. .; TAS. GO: 00:005189; F:peptide hormone; TAS. GO: 00:005180; F:peptide hormone; TAS. GO: 00:006280; P:cell motility; TAS. GO: GO:0006280; P:DNA replication; TAS. GO: 00:000941; P:glycolate metabolism; TAS. GO: GO:0007517; P:muscle development; TAS. GO: GO:0007285; P:RAS protein signal transduction; TAS. GO: GO:0007165; P:RAS protein signal transduction; TAS. GO: GO:0007165; P:RAS protein signal transduction; TAS. GO: GO:0007803; Insulin; Iransduction; TAS. Francero: IPRO0482; Insulin; I.S. Francero: IPRO04825; Insulin; I.S. Francero: IPRO04825; Insulin; I.S. Francero: IRFF. Insulin; I.S. Francero: IRFF. IIGF: I.S. Francero: IIGF: IIGF: I.S. Francero: IIGF: IIGF: I.S. Francero: IIGF: IIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN-LIKE GROWTH FACTOR IB.
                                                                                                                                                -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; E88A8CFBD1CD1873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMOUD(8; 110x, 11)
PROSITE; PSOOGS; INSULIN; 1.
Insulin family; Growth factor; 3D-structure; Plasma;
Alternative splicing; Signal; Polymorphism.
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A -> D (IN dbSNP:6213).
/FTId=VAR_013945.
                                         Event-Alternative splicing; Named isoforms-2;
                                                                                   IsoId-P05019-1; Sequence-Displayed;
                                                                                                                          IsoId-P01343-1; Sequence-External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                      EMBL; M14155; AAA52537.1; -...
EMBL; M12659; AAA52537.1; JOINED.
EMBL; M14154; AAA52537.1; JOINED.
EMBL; M14154; AAA52537.1; JOINED.
EMBL; M1568; AAA52537.1; JOINED.
EMBL; X03420; CAA27250.1; ALT_SEQ.
EMBL; X03420; CAA27152.1; -...
EMBL; X03421; CAA27153.1; -...
EMBL; X03421; CAA27153.1; -...
EMBL; X03421; CAA27153.1; -...
EMBL; X03421; CAA27153.1; -...
SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21841
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R PDB; 2GF1; 15-APR-93.

R PDB; 3GF1; 15-APR-93.

R PDB; 1BOT; 18-MAX-99.

Genew; HGNC: 5464; IGF1.

MIM; 147440;
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118
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49
78
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111
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                                                                                                           Name-IGF-IA;
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PROPEP
DISULFID
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DISULFID
VARIANT
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DOMAIN
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HELIX
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HELIX
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39
380 AA;
                                                                                                                                                                                                                                      NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                       chromosome III.
                                                                                                                                   DDX8_ARATH
 CARBOHYD
           SEQUENCE
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                          clones.
                                                                                                                RESULT 15
DDX8_ARATH
                                                 Matches
 FT
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                    ä
                   Gaps
                                                                                                                                                                                                                        AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PALMITATE (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                    ï
 DB 1; Length 195;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                  8
                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Kappa-type opioid receptor (KOR-1).
                                                                                                      380 AA.
Score 47.5; D
Pred. No. 9.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Lipoprotein; Palmitate.
                                                 || : || | || | ::|
GWPKTHPGGEQKEGTEASLQIR 172
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A55259; A55259.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                    4 GWLRPEDGG-QAEGAEDELEVR 24
37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04092; AAA67171.1; -.
                Conservative
                                                                                                      STANDARD;
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=10141;
                                                                                                      OPRK_CAVPO
                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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CARBOHYD
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                                                                                   RESULT 14
OPRK_CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               038953; 09LRV0;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative pre-mRNA splicing factor ATP-dependent RNA helicase.
AT3G26560 OR MFEI6.8.
AT3G26560 OR MFEI6.8.
Eukaryota; ViridIplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAA RES. 7:131-135(2000).
-!- FUNCTION: COULD ACT LATE IN THE SPLICING OF PRE-MRNA AND MEDIATE
-!- FUNCTION: COULD ACT LATE IN THE SPLICEOSOMES (BY SIMILARITY).
-!- THE RELEASE OF THE SPLICED MRNA FROM SPLICEOSOMES (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
                                                                                                                                                                           Gaps
N-LINKED (GLCNAC. . .) (POTENTIAL).
4FF053834DBBA623 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE-97086629: Pubwed-8932388;
Quigley F., Dao P., Cottet A., Mache R.;
Sequence analysis of an 81 kb contig from Arabidopsis thaliana
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY. DDX8/PRP22 ORTHOLOG. SIMILMSTITY: Conteains 1 S1 motif domain. CAUTION: Rei.1 sequences differ from that shown due to a frameshift in position 57.
                                                                                                 Score 47; DB 1; Length 380;
Pred. No. 22;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 24:4313-4318(1996).
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EMBL; X97970; CAA66613.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-20277480; PubMed-10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB028611, BAB01838.1; -. HSSP; P05055; 1SRO.
InterPro; IPR001410; DEAD.
InterPro; IPR002464; DEAH_box.
InterPro; IPR001650; Helicase_C.
InterPro; IPR003029; S1.
                                                                                                                                                                                                                                                  2 LAGWLRPEDGGQAEGAEDELE 22
                                                                                                                                                                                                                                                                                                                     30 LPGWAEPDGNGSAGPQDEQLE 50
39 N
42736 MW;
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Pfam: PF00575; S1; 1.
SMART: SM00487; DEXDC; 1.
SMART: SM00490; HELICC; 1.
SMART; SM00316; S1; 1.
                                                                                                        37.38;
                                                                                                                                          38.18;
                                                                                                                                      Local Similarity 38.1
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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1;
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PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
PROSITE; PS50126; S1; 1.
Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
ATP-binding; Nuclear protein.
DOMAIN 214 283 MOTIF.
NP_BIND 538 545 ATP (POTENTIAL).
SITE DOMAIN 777 780 POLY-PRO.
SEQUENCE 1168 AA; 134156 MW; B3632DE4A7A7690C CRC64;
                                                                                                                                                             Query Match
37.3%; Score 47; DB 1; Length 1168;
Best Local Similarity 57.9%; Pred. No. 66;
Matches 11; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                     Search completed: September 11, 2003, 17:21:44 Job time : 6.46524 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 11, 2003, 17:21:03 ; Search time 8.98396 Seconds
(without alignments)
256.908 Million cell updates/sec Run on:

US-09-853-253-4 126 1 ALAGWLRPEDGGQAEGAEDELEVR 24 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir_76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qhrelin precursor		nucleoplasmin - Af	probable transcrip	hypothetical prote	conserved hypothet	chloride channel p	chloride channel,	hypothetical prote	amyloid precursor-	amino acid ABC tra	exfoliative toxin	Na+/Ca2+, K+-exchan	hypothetical prote		protein kinase PK1	kappa opioid recep	unknown protein F2	hypothetical prote					protein containing	methionyl-tRNA syn		xylan beta-1,4-xvl	hypothetical prote	matrix metalloprot
SUMMARIES	ID	A59316	931	A26169	683609	T21920	B69811	AE2760	C97541	B75433	A46362	C75609	A26050	S20969	T49338	IGHU1B	T09738	A55259	C96767	T26398	T03975	T21674	A87377	C82965	н97088	AH2760	F97541	C84110	B71039	138028
	DB	-	Н	7	~	7	7	7	7	7	~	7	~	7	7		~	7	7	~	~	~	~	7	7	~	7	~	7	7
	Query Match Length	117	117	200	232	249	91	604	604	131	653	484	274	1199	114	195	355	380	1273	80	740	163	259	287	491	516	516	528	871	582
æ	Query Match	100.0	75.4	42.9	41.3	40.9	40.5	40.5	40.5	39.7	39.7	39.3	38.9	38.9	38.1	37.7	37.3	37.3	37.3	36.9	36.9	36.5	36.5	36.5	36.5		36.5			
	Score	126	95	54	52	51.5	51	51	51	20	S	49.5		49	48	47.5	47	47	47	46.5	ė.	46	46	46	46	46	46	46	46	45.5
	Result No.	-	7	Э	4	S	9	7	<b>œ</b>	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

matrix metalloprot matrix metalloprot cold shock domain ribosomal protein 40s ribosomal prote hypochetical prote cCAAT-binding fact hypothetical prote probable transport cR protein - Dei potassium channel CTP synthase - Dei ATP-binding proteil	ALIGNMENTS  Lin precursor - human terrate names: preproghtelin tectes: Hown sapiens (man) tectes: Hown sapiens tectes: Hown sapie	way rat) islon 16-Jun-2000 #text_change 21-Jul-2000 :: Nakazato, M.; Matsuo, H.; Kangawa, K. none-releasing acylated peptide from stomach. 20067959; PMID:10604470 sptual translation NID:96691569; PIDN:BAA89370.1; PID:96691570 tissue stomach endocrine cells
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0000000000000000	eelin )) tte, Y. tte, Y	(No. 1) (No. 1
588 689 11991 699 694 694 644 644 644 644 644 644 644	sor - human mes: preproghrelin -2000 #sequence_revision 59316 Hosoda, H.; Date, Y.; Nai 6606, 1999 In 16 a growth-hormone-r mber: A59316; MUID:20067 5000	reophresquences against a squences against a squence against a squenc
11777777777777777777777777777777777777	or - huma es: prepr saptens 2000 #seq 2010 #seq 9316 osoda, H. Coton 1 osoda, H. Coton 1 osober: A593 osober:	coursor - rat names: prep Rattus norvep Jun-2000 #se : B59306 [1, Hosoda, H 656-660, 19 : number: A59 : number: A5
44 NN 4444444444444 NNNNNNNNNNNNNNNN	ESULT 1 5916 5916 5916 5916 5916 5916 5916 591	RESULT 2 B59316 Ghrelin precursor - rat N'Alternate names: preproght C; Species: Rattus norvegicus C; Date: 16-Jun-2000 #sequenc C; Accession: B59316 R; KOjima, M.; Hosoda, H.; Da Nature 402, 656-660, 1999 A; Title: Ghrelin is a growth A; Reference number: A59316; A; Accession: B59316 A; Katus: not compared with A; Molecule type: mRNA; prote A; Residues: 1-117 <koj> A; Cross-references: GB:AB022 A; Experimental source: straia</koj>
0 M B B B B B B B B B B B B B B B B B B	AESULT 1 A59116 ghrelin precursor - hum N.Alternate names: prept C.Species: Homo saplens C.Date: 16-Jun-2000 #se C.Accession: A59316 R.Kojima, M.; Hosoda, H Nature 402, 656-660, A.Title: Ghrelin is a g A.Reference number: A59 A.Accession: A59316 A.Status: not compared A.Molecule type: mRNA A.Residues: 1-117 <koja 1-23="" 26="" a.cross="" a.experimental="" a.note:="" alagwlrpp<="" best="" blinding="" c.comment:="" c.keywords:="" c.superfamily:="" db="" domain:="" gb:="" ghrelin="" hormone;="" life:="" local="" match="" motilin="" octa="" ouery="" references:="" s.2="" secre="" sep:="" signal="" similarity="" site:="" source:="" submittee:="" td=""><td>RESULT B59316 ghrelin N; Alter: C; Speci C; Cate: C; Acces R; Kojim R, Title A; Title A; Refer A; Refer A; Refer A; Resid A; Resi</td></koja>	RESULT B59316 ghrelin N; Alter: C; Speci C; Cate: C; Acces R; Kojim R, Title A; Title A; Refer A; Refer A; Refer A; Resid A; Resi

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C; Accession: B69811
R; Kunst, F: Ogasawara, N: Moszer, I:; Albertini, A.M.; Alloni, G; Azevedo, V.; Ber C; Euron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, Nature 390, 240-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Kuthors: Foulger, D.; Fritz, C.; Fujita, M.; Evijita, K.; Lapidus, A.; Lardino, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Msauda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanla, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanla, A; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanla, A; Authors: Schlaich, S.; Schocher, R.; Scoffone, F.; Seklayochi, J.; Schowska, A.; Outhya T.; Winters, P.; Wipat, A.; Tamanco, H.; Ta
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z75540; PIDN:CAA99852.1; GSPDB:GN00019; CESP:F37D6.7
A;Experimental source: clone F37D6
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                                                                                                                       hypothetical protein F37D6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21920
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C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein yflL - Bacillus subtilis
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                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, June 1996
A:Reference number: 219487
A:Accession: T21920
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-249 <WILD
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5; Mismatches
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73 WIRPETNGGDDDGSEDK 89
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Best Local Similarity 44.0%;
Matches 11; Conservative 5
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C;Superfamily: acylphosphatase
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Cyaccession: 683609
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: G83609
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-232 <STO>
A; Note: submitted to GenBank, June 1999
C; Comment: Ghreiin secreted by the stomach stimulates the release of somatotropin (growt C; Superfamily: motilin
C; Keywords: hormone; lipoprotein; stomach
C; Keywords: hormone; lipoprotein; stomach
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-51/Product: ghrelin #status predicted <AMIT>
F; 24-51/Product: ghrelin #status predicted <AMIT>
F; 24-51/Product: cortanoate (Ser) (covalent) #status sexperimental
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999
CiAccession: A26169
CiAccession: A26169
Ci 69-74, 1987
Ci Dilworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.
EMBO J. 6, 69-74, 1987
A;Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of shacession: A26169; MUID:87218476; PMID:2884102
A;Reference number: A26169
A;Reference number: A26169
A;Residues: 1-200 <DIN>
A;Residues: 1-200 <DIN>
A;Residues: 1-200 <DIN>
CiSuperfamily: nucleophosmin
C;Reywords: molecular chaperone; nucleus
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                                                                                                                                                                                                                                                                                                                                      75.4%; Score 95; DB 1; Length 117; 75.0%; Pred. No. 2.6e-06; tive 2; Mismatches 4; Indels
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72.7%; Pred. No. 6.2;
.ive 2; Mismatches
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C;Genetics:
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Best Local Similarity 75.05
Matches 18; Conservative
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202 GWLRPQDGSRA 212
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GB:AE000513; NID:g6458869; PIDN:AAF10714.1; PID:g645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Musculus (house mouse)
C;Accession: A46362; Musculus (house mouse)
R;Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F. Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A;Titles: Identification of a mouse brain cDNA that encodes a protein related to the A;Reference number: A46362; MuID:93066322; PMID:1279693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBIP:118684)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C;Keywords: transmembrane protein
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       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 CWH.
A;Kesidues: 1-131 CWH.
A;Cross-references: GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AA
A;Experimental source: strain R1
C;Genetics:
A;Genee: DR1139
A;Gene: DR1139
C;Superfamily: Deinococcus radiodurans hypothetical protein DR1139
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Pred. No. 34;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             Score 50; DB Pred. No. 6.7; 2; Mismatches
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Best Local Similarity 61.1%;
Matches 11; Conservative
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ilarity 47.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: nucleic acid
A; Residues: 1-653 <WAS>
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Best Local Similarity
9; Conserve
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Best Local Similarity
Matches 10; Conserva
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A; Residues: 1-484 <WHI>
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A; Status: preliminary
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A;Gene: DRA0136
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chloride channel, clc (AE005067) [imported] - Agrobacterium tumefaciens (strain C58, 67.5pc-6128: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Accession: C97541
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm. A.: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A; Tille: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97559; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: B75433
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Snith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10557266
                                                                                                                                                                                                                                                                                                                     ster, E.W.

A;Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: A52760

A;Status: preliminary

A;Molecule type: DNA
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A. Cross-references: GB. AE008688; PIDN: AAL42499.1; PID: g17739917; GSPDB: GN00186
A. Experimental source: strain C58 (Dupont)
C. Genetics:
A. Genetics:
A. Senetics:
A. Senet
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A,Molecule type: DNA
A,Residues: 1-604 <KUR>
A,Cross-references: GB:AE007869; PIDN:AAK87284.1; PID:g15156576; GSPDB:GN00169
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ed. No. 22;
Mismatches
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illarity 62.5%; Pred. No.
Conservative 1; Mismatc
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A; Experimental source: anaplastic oligodedroglioma
A; Note: sequence modified after extraction from NCBI backbone
A; Note: sequence modified after extraction from NCBI backbone
A; Note: sequence extracted from NCBI backbone (NCBIN:133058)
B; Stegfried, J.M.; Rasprzyk, P.G.; Treston, A.M.; Mulshine, J.L.; Quinn, K.A.; Cuttit Proc. Natl. Acad. Sci. U.S.A. 89, 8107-8111, 1992
A; Titler: A mitograin peptide amide enroaded within the E peptide domain of the insulin A; Reference number: A42664; MUID:92390398; PMID:1325646
A; Contents: annotation; IBB-1; amidated carboxyl end
C; Comment: For an alternative splice form, see PIR:IGHUI.
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A; Residues: 1-195 <SNA
A; Cross-references: EMBL:X56774; NID:932991; PIDN:CAA40093.1; PID:932992
A; Cross-references: EMBL:X56774; NID:932991; PIDN:CAA40093.1; PID:932992
R; Sandberg-Nordqvist, A.C.; Stahlbom, P.A.; Reinecke, M.; Collins, V.P.; von Holst, H
Cancer Res. 53, 2478-2478, 1993
A; Title: Characterization of insulin-like growth factor 1 in human primary brain tumo
A; Reference number: A48960; MUID:93265440; PMID:8495408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nylternate names: IGF-IB; somatomedin C
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Accession: A01611; A26181; S30540; B48960; A42664
R; Rotwein, P:; Pollock, K. M.; Didler, D.K.; Krivi, G.G.
A; Title: Organization and sequence of the human insulin-like growth factor I gene. Al
A; Reference number: A92581; MUID:86168194; PMID:2937782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Two insulin-like growth factor I messenger RNAs are expressed in human liver A;Reference number: A26181; MUID:86094355; PMID:3455760
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A; Residues: 1-195 <RQT2>
A; Cross-references: GB:M1568; NID:g183111; PIDN:AAA52539.1; PID:g183112
A;Cross-references: GB:M1568; NID:g183111; PIDN:AAA52539.1; PID:g183112
R;Sandberg Nordqvist, A.C.; Stahlbom, P.A.; Lake, M.; Sara, V.R.
submitted to the EMBL Data Library, November 1990
A; Description: Uncleotide sequence of the human fetal brain IGF-1b.
A; Reference number: $30540
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                        A;Gene: NCSP:B13N20.230
A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B13N20.230
                                                                                                                                                                                               Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1-21/Domain: signal sequence #status predicted </F;22-48/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                           Score 48; DB 2
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77-81, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:120081; OMIM:147440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rotwein, P.
Proc. Natl. Acad. Sci. U.S.A. 83,
                                                                                                                                                                                           38.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                       9 EDGGQAEGAEDELEV 23
                                                                                                                                                                                                                                    Best_Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 12q22-12q24.1
A; Introns: 21/3; 74/1; 134/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-195 <ROT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-195 <SA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B48960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A01611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A26181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: IGF1
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                              δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Na+Ca2+,K+-exchanging protein - bovine
Na+Ca2+,K+-exchanger
Ns+Aternate names: Na+/Ca2+,K+ antiporter;
NsAternate names: Na+/Ca2+,K+ antiporter;
C:Species: Bos primigentus taurus (cattle)
C:Species: Bos primigentus taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S20969
R:Rellaender, H:, Achilles, A:; Friedel, U:; Maul, G.; Lottspeich, F.; Cook, N.J.
EMBO J. 11, 1689-1695, 1992
A:Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovint A; Reference number: S20969; MuID:92258377; PMID:1582405
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B13N20.230 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: 149338
R;Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                             ### State to the control of the cont
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A;Residues: 1-1199 <REI>
A;Cross-references: GB:X66481; NID:9505578; PIDN:CAA47108.1; PID:9505579
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A;Residues: 1-114 <SCH>
A;Cross-references: EMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.230
A;Experimental source: BAC clone B13N20; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1199;
86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2; Length 274; Pred. No. 19; 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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1larity 42.9%; Pred. No. 86;
Conservative 6; Mismatches
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                                                                                 86 WLKIQDGGDTTGQEEQPE 103
                                LAGWLRPEDGGQAEGAED 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 WLRPEDGGQAEGAEDELE 22
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ilarity 44.4%;
Conservative
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Best Local Similarity
Thes 8; Conserva
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Les 9; Conserv
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A; Status: preliminary
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Matches
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F:49-118/Product: insulin-like growth factor I *status predicted <MAT>
F:49-77/Domain: insulin chain B-like *status predicted <CHB>
F:49-77/Domain: insulin connecting C peptide-like *status predicted <CHC>
F:78-89/Domain: insulin connecting C peptide-like *status predicted <CHC>
F:90-110/Domain: insulin chain A-like *status predicted <CHA>
F:111-118/Domain: insulin chain A-like *status predicted <CHD>
F:111-118/Domain: carboxyl-terminal propeptide (E peptide) *status predicted <CHE>
F:151-172/Product: insulin-like growth factor IB-El amide *status predicted <MA2>
F:54-96,66-109,95-100/Disulfide bonds: *status predicted
F:172/Modified site: amidated carboxyl end (Arg) (amide in mature form from following 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

37.7%; Score 47.5; DB 1; Length 195;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 8; Indels
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